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  * * * * * * * * * * * * * * STN  Columbus  * * * * * * * * * * * * * * *

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FILE COVERS 1907 - 8 Jan 2004 VOL 140 ISS 3
FILE LAST UPDATED: 8 Jan 2004  (20040108/ED)

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  substance identification.


=> s desorption(w)spectrometry
         91306 DESORPTION
        295803 SPECTROMETRY
L1         285 DESORPTION(W)SPECTROMETRY

=> s l1 and diagnostic(w)marker?
         68256 DIAGNOSTIC
        151493 MARKER?
          1458 DIAGNOSTIC(W)MARKER?
L2           0 L1 AND DIAGNOSTIC(W)MARKER?

=> s l1 and substrate?
        850699 SUBSTRATE?
L3          34 L1 AND SUBSTRATE?

=> s l3 and disease?
        722093 DISEASE?
L4           1 L3 AND DISEASE?


=> d his

     (FILE 'HOME' ENTERED AT 18:27:05 ON 11 JAN 2004)

     FILE 'CA' ENTERED AT 18:27:13 ON 11 JAN 2004
L1          285 S DESORPTION(W)SPECTROMETRY
L2            0 S L1 AND DIAGNOSTIC(W)MARKER?
L3           34 S L1 AND SUBSTRATE?
L4            1 S L3 AND DISEASE?

=> s l1 and detect?
       1268836 DETECT?
L5          31 L1 AND DETECT?

=> s l5 not l3
L6          27 L5 NOT L3

=> s l6 not l4
L7          27 L6 NOT L4


STN INTERNATIONAL LOGOFF AT 18:41:13 ON 11 JAN 2004
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COST IN U.S. DOLLARS                                    SINCE FILE      TOTAL
                                                           ENTRY    SESSION
FULL ESTIMATED COST                                         0.21       0.21

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FILE COVERS 1907 - 8 Jan 2004 VOL 140 ISS 3
FILE LAST UPDATED: 8 Jan 2004  (20040108/ED)

  This file contains CAS Registry Numbers for easy and accurate
  substance identification.


=> s surface(w)enhanced(w)neat(w)desorption
      1774339 SURFACE
       408771 ENHANCED
        10976 NEAT
        91306 DESORPTION
L1          1 SURFACE(W)ENHANCED(W)NEAT(W)DESORPTION

=> d all

L1   ANSWER 1 OF 1  CA  COPYRIGHT 2004 ACS on STN
AN   119:176946  CA
ED   Entered STN:  30 Oct 1993
TI   New desorption strategies for the mass-spectrometric analysis of
     macromolecules
AU   Hutchens, T. William; Yip, Tai Tung
CS   Dep. Pediatr., Baylor Coll. Med., Houston, TX, 77030, USA
SO   Rapid Communications in Mass Spectrometry (1993), 7(7), 576-80
     CODEN: RCMSEF; ISSN: 0951-4198
DT   Journal
LA   English
CC   9-5 (Biochemical Methods)
     Section cross-reference(s): 6, 73
AB   Two new desorption strategies are based on the mol. design and
     construction of two general classes of sample 'probe' surfaces.  The first
     class of surfaces is designed to enhance the desorption of intact
     macromols. presented alone (neat) to the surface; the authors call this
       ***surface***  -  ***enhanced***     ***neat***     ***desorption***
     (SEND).  The availability of probe surfaces derivatized with, or composed
     of, multiple types and defined nos. of energy-absorbing mols. will
     facilitate investigations of energy transfer and desorption/ionization
     mechanisms.  The second class of probe surfaces is designed to enhance the
     desorption of specific macromols. captured directly from unfractionated
     biol. fluids and exts.; the authors call this surface-enhanced affinity
     capture (SEAC).  Use of these new probe surfaces as chem. defined
     solid-phase reaction centers will facilitate protein discovery through
     mol. recognition in situ and also macromol. structure anal. through the
     sequential chem. and/or enzymic modification of the adsorbed analyte in
     situ.  Specific examples of laser-assisted SEND and SEAC time-of-flight
     mass spectrometry are presented to illustrate the potential for increased
     selectivity, analyte detection sensitivity, and mass measurement accuracy.
ST   macromol biol desorption mass spectrometry; biopolymer mass spectrometry
     desorption
```

Glycopeptides
Glycoproteins, properties
Proteins, properties
RL: PRP (Properties)
(mass spectrometry of, desorption methods for)
IT Mass spectrometry
(of biomacromols., new desorption strategies for)
IT Glass, oxide
Polyamide fibers, uses
RL: ANST (Analytical study)
(probe, for mass spectrometry of macromols.)
IT Macromolecular compounds
RL: PRP (Properties)
(biol., mass spectrometry of, desorption methods for)
IT 28166-41-8, .alpha.-Cyano-4-hydroxycinnamic acid
RL: ANST (Analytical study)
(in mass spectrometry of biol. macromols.)
IT 530-59-6, Sinapinic acid
RL: ANST (Analytical study)
(matrix, for mass spectrometry of biol. macromols.)
IT 9003-07-0, Polypropylene 9003-53-6, Polystyrene
RL: ANST (Analytical study)
(probe, for mass spectrometry of macromols.)

=> s surface(w)enhanced(w)laser(w)desorption(w)ionization
1774339 SURFACE
408771 ENHANCED
416640 LASER
91306 DESORPTION
227296 IONIZATION
L2 118 SURFACE(W)ENHANCED(W)LASER(W)DESORPTION(W)IONIZATION

=> s l2 and diagnostic
68256 DIAGNOSTIC
L3 20 L2 AND DIAGNOSTIC

=> d all 1-20

L3 ANSWER 1 OF 20 CA COPYRIGHT 2004 ACS on STN
AN 139:321232 CA
ED Entered STN: 13 Nov 2003
TI Putative protein markers in the sera of men with prostatic neoplasms
AU Lehrer, S.; Roboz, J.; Ding, H.; Zhao, S.; Diamond, E. J.; Holland, J. F.; Stone, N. N.; Droller, M. J.; Stock, R. G.
CS Department of Radiation Oncology, Mount Sinai School of Medicine, New York, NY, USA
SO BJU International (2003), 92(3), 223-225
CODEN: BJINFO; ISSN: 1464-4096
PB Blackwell Publishing Ltd.
DT Journal
LA English
CC 14-1 (Mammalian Pathological Biochemistry)
AB OBJECTIVE To describe the preliminary identification of serum proteins that may be ***diagnostic*** markers in prostate cancer. PATIENTS AND METHODS The study included 11 men referred for treatment of localized prostate cancer, 12 with benign prostatic hyperplasia (BPH) and 12 disease-free controls. For serum protein anal., the protein-chip array ***surface*** - ***enhanced*** ***laser*** ***desorption*** / ***ionization*** (SELDI) technique was used (Ciphergen Biosystems, Fremont, CA). SELDI combines protein-chip technol. with time-of-flight mass spectrometry, and offers the advantages of speed, simplicity and sensitivity. RESULTS Three protein peaks were identified in the serum of men with prostate cancer and BPH, but not in controls, with relative mol. masses of 15.2, 15.9 and 17.5 kDa. These three proteins were significantly assocd. with BPH and prostate cancer when compared with controls (P = 0.001, 0.004, and 0.011, resp., Kruskal-Wallis test). Interestingly, the 17.5 kDa protein was more abundant in five men with stage T1 prostate cancer than in eight with stage T2 (P= 0.016, two tailed Mann-Whitney U-test cor. for ties). CONCLUSIONS These proteins, particularly the 15.9 kDa one, may be used for the diagnosis or monitoring of prostate cancer and differentiation from BPH, and have the potential for antibody-based chip SELDI-TOF technol. Identified proteins may be targets for immunotherapy.
ST prostate cancer serum protein tumor marker

RL: BSU (Biological study, unclassified); DGN (Diagnostic use); BIOL (Biological study); USES (Uses)
(15.2 kDa; putative protein markers in the sera of men with prostatic neoplasms)
IT Proteins
RL: BSU (Biological study, unclassified); DGN (Diagnostic use); BIOL (Biological study); USES (Uses)
(15.9 kDa; putative protein markers in the sera of men with prostatic neoplasms)
IT Proteins
RL: BSU (Biological study, unclassified); DGN (Diagnostic use); BIOL (Biological study); USES (Uses)
(17.5 kDa; putative protein markers in the sera of men with prostatic neoplasms)
IT Proteins
RL: BSU (Biological study, unclassified); DGN (Diagnostic use); BIOL (Biological study); USES (Uses)
(blood; putative protein markers in the sera of men with prostatic neoplasms)
IT Human
Prostate gland, neoplasm
Tumor markers
(putative protein markers in the sera of men with prostatic neoplasms)
RE.CNT 7 THERE ARE 7 CITED REFERENCES AVAILABLE FOR THIS RECORD
RE
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L3 ANSWER 2 OF 20 CA COPYRIGHT 2004 ACS on STN
AN 139:229066 CA
ED Entered STN: 02 Oct 2003
TI Macrophage proteomic fingerprinting predicts HIV-1-associated cognitive impairment
AU Luo, X.; Carlson, K. A.; Wojna, V.; Mayo, R.; Biskup, T. M.; Stoner, J.; Anderson, J.; Gendelman, H. E.; Melendez, L. M.
CS Department of Neurology, First China Hospital Medical University, Shenyang, Peop. Rep. China
SO Neurology (2003), 60(12), 1931-1937
CODEN: NEURAI; ISSN: 0028-3878
PB Lippincott Williams & Wilkins
DT Journal
LA English
CC 15-8 (Immunochemistry)
AB Background: Specific proteins produced from monocytes may be linked to the pathogenesis and aid in the diagnosis of HIV-1-assocd. dementia (HAD). Objective: The authors assessed whether a ***diagnostic*** phenomic protein profile could be obtained from monocyte-derived macrophages (MDM) from HIV-1-infected patients with cognitive impairment. Methods: Twenty-one HIV-1-infected Hispanic women and 10 seroneg. controls matched by age and sex were followed at the University of Puerto Rico Medical Sciences Campus, where neuropsychol., immune, and viral parameters were tested. Monocytes were recovered by Percoll gradient centrifugation from peripheral blood mononuclear cells. MDM lysates were prepd. after 7 days of cultivation and protein profiles analyzed by ***surface*** ***enhanced*** ***laser*** ***desorption*** / ***ionization*** (SELDI)-time of flight (TOF) ProteinChip tests. Classification trees were prepd. for statistical analyses. Results: A total of 177 protein peaks from 2 to 80 kDa were evaluated in 31 patient MDM lysates by SELDI-TOF ProteinChip assays. Select protein peaks, at 5028 and 4320 Da, sepd. HIV-1-infected from HIV-1-seroneg. subjects with a sensitivity of 100% and a specificity of 80%. Thirty-eight peaks were used to differentiate HIV-1-infected subjects with and without cognitive impairment. A 4348 Da protein sepd. the two groups with a sensitivity of 100% and a specificity of 75%. Conclusions: The identification of unique phenomic MDM profiles from cognitively impaired HIV-1-infected patients supports the hypothesis that changes in monocyte function parallel the development of HAD.
ST monocyte protein proteomic fingerprinting HIV dementia
IT Mental disorder
(dementia, HIV-assocd.; macrophage proteomic fingerprinting predicts HIV-1-assocd. cognitive impairment)
IT Human

Macrophage
(macrophage proteomic fingerprinting predicts HIV-1-assocd. cognitive impairment)
IT Proteins
RL: ADV (Adverse effect, including toxicity); BIOL (Biological study)
(macrophage proteomic fingerprinting predicts HIV-1-assocd. cognitive impairment)
RE.CNT 36 THERE ARE 36 CITED REFERENCES AVAILABLE FOR THIS RECORD
RE
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L3 ANSWER 3 OF 20 CA COPYRIGHT 2004 ACS on STN
AN 139:228668 CA
ED Entered STN: 02 Oct 2003
TI A panel of cerebrospinal fluid potential biomarkers for the diagnosis of Alzheimer's disease
AU Carrette, Odile; Demalte, Isabelle; Scherl, Alexander; Yalkinoglu, Oezkarn; Corthals, Garry; Burkhard, Pierre; Hochstrasser, Denis F.; Sanchez, Jean-Charles
CS Biomedical Proteomics Research Group, Central Clinical Chemistry Laboratory, Geneva University Hospital, Geneva, Switz.
SO Proteomics (2003), 3(8), 1486-1494
CODEN: PROTC7; ISSN: 1615-9853
PB Wiley-VCH Verlag GmbH & Co. KGaA
DT Journal
LA English
CC 14-10 (Mammalian Pathological Biochemistry)
AB The diagnosis of Alzheimer's disease (AD), the most common form of dementia in the general population, usually relies upon the presence of typical clin. features and structural changes on brain magnetic resonance imaging. Over the last decade, a no. of biol. abnormalities have been reported in the cerebrospinal fluid (CSF) of AD patients, in particular altered levels of the tau protein and the 1-42 fragment of the amyloid precursor protein. These, however, have not yet proved sensitive and specific enough to be included in the ***diagnostic*** criteria for AD, leaving plenty of room for the search of novel biomarkers. The present study describes the anal. of CSF polypeptides by a protein-chip array technol. called ***surface*** ***enhanced*** ***laser*** ***desorption*** / ***ionization*** -time of flight-mass spectrometry (SELDI-TOF-MS). Using this approach, we detected statistically

one underexpressed polypeptides in the CSF of AD patients as compared to healthy controls. Four of them were further purified by strong anionic exchange chromatog. (SAX) and identified by MS anal. as cystatin C, two .beta.-2-microglobulin isoforms, an unknown 7.7 kDa polypeptide, and a 4.8 kDa VGF polypeptide. The combination of the five polypeptides for the diagnosis of AD allowed to classified six AD patients out of the nine included in this study and all the ten controls, which means in this small cohort that the specificity and sensitivity are 100% and 66%, resp. This study, based on the protein-chip array technol., demonstrates the presence in the CSF of novel potential biomarkers for AD, which may be used for the diagnosis and perhaps the assessment of the severity and progression of the disease.

ST cerebrospinal fluid biomarker Alzheimer disease diagnosis

IT Proteins
RL: BSU (Biological study, unclassified); DGN (Diagnostic use); BIOL (Biological study); USES (Uses)
(7700-mol.-wt.; panel of cerebrospinal fluid potential biomarkers for diagnosis of Alzheimer's disease)

IT Proteins
RL: BSU (Biological study, unclassified); DGN (Diagnostic use); BIOL (Biological study); USES (Uses)
(VGF; panel of cerebrospinal fluid potential biomarkers for diagnosis of Alzheimer's disease)

IT Alzheimer's disease
Biomarkers (biological responses)
Cerebrospinal fluid
Diagnosis
Human
(panel of cerebrospinal fluid potential biomarkers for diagnosis of Alzheimer's disease)

IT Microglobulins
RL: BSU (Biological study, unclassified); DGN (Diagnostic use); BIOL (Biological study); USES (Uses)
(.beta.2-, isoforms; panel of cerebrospinal fluid potential biomarkers for diagnosis of Alzheimer's disease)

IT 91448-99-6, Cystatin C
RL: BSU (Biological study, unclassified); DGN (Diagnostic use); BIOL (Biological study); USES (Uses)
(panel of cerebrospinal fluid potential biomarkers for diagnosis of Alzheimer's disease)

RE.CNT 30 THERE ARE 30 CITED REFERENCES AVAILABLE FOR THIS RECORD

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L3 ANSWER 4 OF 20 CA

AN 139:145892 CA

ED Entered STN: 28 Aug 2003

AU Tomosugi, Naohisa
CS Div. Nephrol., Dep. Intern. Med., Kanazawa Med. Univ., Japan
SO Seibutsu Butsuri Kagaku (2003), 47(1,2), 17-22
CODEN: SBBKA4; ISSN: 0031-9082
PB Nippon Denki Eido Gakkai
DT Journal; General Review
LA Japanese
CC 9-0 (Biochemical Methods)
Section cross-reference(s): 14
AB A review. Needle biopsy is the std. test for the diagnosis of renal diseases. Biopsy-assocd. complications could not be eliminated in spite of recent refinement. The development of noninvasive ***diagnostic*** test that provides insights into the mechanisms of renal diseases would be expected. Recently the advent of SELDI-TOF-MS (***surface*** - ***enhanced*** ***laser*** ***desorption*** / ***ionization*** time-of-flight mass spectrometry) has extended the application of mass spectrometry to the study of proteins from complex biol. systems. We applied the new protein-chip technol. based on SELDI in a discovery of renal disease biomarkers. Proteomic patterns in serum by means of protein-chip were exemplified by elucidating a biomarker candidate for acute renal allograft rejection. In discovery phase protein profiles for control and rejection were compared in protein expression. The process of characterization and validation for the biomarker could be monitored by MS detection. SELDI protein-chip technol. will be applied more frequently to a no. of medical and basic research problems because of high resoln., high reproducibility, ease of use, and femtomole sensitivity.
ST review renal disease biomarker screening ProteinChip System; SELDI mass spectrometry renal disease protein screening review
IT Laser ionization mass spectrometry
(photodesorption, surface-enhanced, time-of-flight; screening of biomarkers in renal diseases by ProteinChip System based on SELDI-TOF mass spectrometry for proteins trapped on affinity chips)
IT Laser desorption mass spectrometry
(photoionization, surface-enhanced, time-of-flight; screening of biomarkers in renal diseases by ProteinChip System based on SELDI-TOF mass spectrometry for proteins trapped on affinity chips)
IT Biomarkers (biological responses)
Human
Kidney, disease
Protein microarray technology
(screening of biomarkers in renal diseases by ProteinChip System based on SELDI-TOF mass spectrometry for proteins trapped on affinity chips)
IT Proteins
RL: ANT (Analyte); DGN (Diagnostic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(screening of biomarkers in renal diseases by ProteinChip System based on SELDI-TOF mass spectrometry for proteins trapped on affinity chips)

L3 ANSWER 5 OF 20 CA COPYRIGHT 2004 ACS on STN
AN 139:115954 CA
ED Entered STN: 14 Aug 2003
TI Analysis of complex autoantibody repertoires by ***surface*** - ***enhanced*** ***laser*** ***desorption*** / ***ionization*** -time of flight mass spectrometry
AU Grus, Franz H.; Joachim, S. C.; Pfeiffer, Norbert
CS Department of Ophthalmology, University of Mainz, Mainz, Germany
SO Proteomics (2003), 3(6), 957-961
CODEN: PROTC7; ISSN: 1615-9853
PB Wiley-VCH Verlag GmbH & Co. KGaA
DT Journal
LA English
CC 15-1 (Immunochemistry)
AB Normal sera contain a large no. of naturally occurring autoantibodies which can mask important disease-assocd. ones. Western blotting has evolved as the most important tool to demonstrate autoantibodies in autoimmune diseases, because of its ability to simultaneous screening for a wide spectrum of different antigens. In previous studies we have shown the ***diagnostic*** potential of the anal. of autoantibodies in autoimmune diseases by means of multivariate statistics and artificial neural networks. However, the Western blotting procedure remains very time-consuming and is also limited in sensitivity. Therefore, we used an on-chip approach for the anal. of autoantibodies. This ProteinChip system uses ProteinChip arrays and SELDI-TOF MS (***surface*** - ***enhanced*** ***laser*** ***desorption*** / ***ionization*** -time of flight mass spectrometry) technol. for capturing, detection, and anal. of proteins without labeling or without the need of chem.

very small quantities of proteins. In the present study, we used arrays with biol. activated surfaces that permit antibody capture studies. Protein-A-Chips were incubated with sera of patients (n = 12). After washing, the chips were incubated with a complex soln. of autoantigens and subsequently washed again. If the Protein-A bound autoantibodies recognized their antigens, these proteins could be sepd. by their mol. masses and were to be detected by mass spectrometry. Previous studies using monoclonal antibodies have demonstrated that the detection limit is in the attomole level. Furthermore, all sera were analyzed by conventional Western blotting for direct comparison. In the present study, we have shown complex on-chip antibody-antigen reactions. At higher mol. wts. (>30 kDa) the detection sensitivity of this onchip method was comparable to conventional Western blotting. At lower mol. mass, the Western blot technique is easily exceeded by the on-chip method. Considering that this on-chip procedure is quite easy to use, is much less time-consuming than Western blotting, and is much more sensitive at least in the low mol. wt. range, the SELDI-TOF technol. is a very promising approach for the screening of autoantibodies in autoimmune diseases. Due to its versatility, this on-chip technol. could allow the large-scale screening for complex autoantibody distributions for ***diagnostic*** purposes and early detection of autoimmune diseases might be possible.

ST autoantibody analysis laser desorption mass spectrometry

IT Blood analysis
Human
Laser desorption mass spectrometry
Time-of-flight mass spectrometry
(anal. of complex autoantibody repertoires by ***surface*** - ***enhanced*** ***laser*** ***desorption*** / ***ionization*** -time of flight mass spectrometry)

IT Autoimmune disease
(anal. of complex autoantibody repertoires by ***surface*** - ***enhanced*** ***laser*** ***desorption*** / ***ionization*** -time of flight mass spectrometry in)

IT Antibodies
RL: ANT (Analyte); ANST (Analytical study)
(autoantibodies; anal. of complex autoantibody repertoires by ***surface*** - ***enhanced*** ***laser*** ***desorption*** / ***ionization*** -time of flight mass spectrometry)

IT Antigens
RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses)
(autoantigens; anal. of complex autoantibody repertoires by ***surface*** - ***enhanced*** ***laser*** ***desorption*** / ***ionization*** -time of flight mass spectrometry and reactivity with)

RE.CNT 19 THERE ARE 19 CITED REFERENCES AVAILABLE FOR THIS RECORD

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L3 ANSWER 6 OF 20 CA COPYRIGHT 2004 ACS on STN
AN 139:81483 CA
ED Entered STN: 31 Jul 2003
TI Proteomic evaluation of archival cytologic material using SELDI affinity mass spectrometry: potential for ***diagnostic*** applications

AU Fetsch, Patricia A.; Simone, Nicole L.; Bryant-Greenwood, Peter K.; Marincola, Francesco M.; Filie, Armando C.; Petricoin, Emmanuel F.; Liotta, Lance A.; Abati, Andrea
CS Laboratory of Pathology, Food and Drug Administration, Bethesda, MD, USA

SO American Journal of Clinical Pathology (2002), 118(6), 870-876

PB American Society of Clinical Pathologists
DT Journal
LA English
CC 9-5 (Biochemical Methods)
Section cross-reference(s): 14
AB Proteomic studies of cells via ***surface*** - ***enhanced*** ***laser*** ***desorption*** / ***ionization*** spectrometry (SELDI) anal. have enabled rapid, reproducible protein profiling directly from crude samples. We applied this technique to archival cytol. material to det. whether distinct, reproducible protein fingerprints could be identified for potential ***diagnostic*** purposes in blinded specimens. Rapid Romanowsky-stained cytocentrifuged specimens from fine-needle aspirates of metastatic malignant melanoma (with both known cutaneous primary and unknown primary sites), clear cell sarcoma, and renal cell carcinoma and reactive effusions were examd. using the SELDI technol. A unique characteristic fingerprint was identified for each disease entity. Fifteen "blinded" unknown samples then were analyzed. When the protein profile fingerprints were plotted against the known fingerprints for the aforementioned diagnoses, the appropriate match or diagnosis was obtained in 13 (87%) of 15 cases. These preliminary findings suggest a substantial potential for SELDI applications to specific pathol. diagnoses.
ST proteomic evaluation neoplasm SELDI mass spectrometry diagnosis; protein neoplasm SELDI diagnosis
IT Sarcoma
(clear cell; proteomic evaluation of archival cytol. neoplasmic material using SELDI affinity mass spectrometry in relation to ***diagnostic*** applications)
IT Body fluid
(effusion; proteomic evaluation of archival cytol. neoplasmic material using SELDI affinity mass spectrometry in relation to ***diagnostic*** applications)
IT Melanoma
(metastatic malignant; proteomic evaluation of archival cytol. neoplasmic material using SELDI affinity mass spectrometry in relation to ***diagnostic*** applications)
IT Laser ionization mass spectrometry
(photodesorption, surface-enhanced; proteomic evaluation of archival cytol. neoplasmic material using SELDI affinity mass spectrometry in relation to ***diagnostic*** applications)
IT Laser desorption mass spectrometry
(photoionization, surface-enhanced; proteomic evaluation of archival cytol. neoplasmic material using SELDI affinity mass spectrometry in relation to ***diagnostic*** applications)
IT Proteome
RL: ANT (Analyte); DGN (Diagnostic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(proteomics; proteomic evaluation of archival cytol. neoplasmic material using SELDI affinity mass spectrometry in relation to ***diagnostic*** applications)
IT Kidney, neoplasm
(renal cell carcinoma; proteomic evaluation of archival cytol. neoplasmic material using SELDI affinity mass spectrometry in relation to ***diagnostic*** applications)
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L3 ANSWER 7 OF 20 CA COPYRIGHT 2004 ACS on STN
AN 138:299912 CA
ED Entered STN: 08 May 2003
TI Clinical potential of proteomics in the diagnosis of ovarian cancer
AU Ardekani, Ali M.; Liotta, Lance A.; Petricoin, Emanuel, III
CS Proteomics Unit, Bethesda, MD, 20892, USA
SO Expert Review of Molecular Diagnostics (2002), 2(4), 312-320
CODEN: ERMDCW; ISSN: 1473-7159
PB Future Drugs Ltd.
DT Journal; General Review
LA English
CC 9-0 (Biochemical Methods)
AB A review. The need for specific and sensitive markers of ovarian cancer is crit. Finding a sensitive and specific test for its detection has an important public health impact. Currently, there are no effective screening options available for patients with ovarian cancer. CA-125, the most widely used biomarker for ovarian cancer, does not have a high pos. predictive value and it is only effective when used in combination with other ***diagnostic*** tests. However, pathol. changes taking place within the ovary may be reflected in biomarker patterns in the serum. Combination of mass spectra generated by new proteomic technologies, such as ***surface*** - ***enhanced*** ***laser*** ***desorption*** ***ionization*** time-of-flight (SELDI-TOF) and artificial-intelligence-based informatic algorithms, have been used to discover a small set of key protein values and discriminate normal from ovarian cancer patients. Serum proteomic pattern anal. might be applied ultimately in medical screening clinics, as a supplement to the ***diagnostic*** work-up and evaluation.
ST review proteomics diagnosis ovarian cancer
IT Diagnosis
Human
Mass spectrometry
Ovary, neoplasm
(clin. potential of proteomic technologies in diagnosis of ovarian cancer)
IT CA 125 (carbohydrate antigen)
RL: DGN (Diagnostic use); BIOL (Biological study); USES (Uses)
(clin. potential of proteomic technologies in diagnosis of ovarian cancer)
IT Algorithm
(genetic; clin. potential of proteomic technologies in diagnosis of ovarian cancer)
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L3 ANSWER 8 OF 20 CA COPYRIGHT 2004 ACS on STN
AN 138:35534 CA
ED Entered STN: 16 Jan 2003
TI Analysis of microdissected prostate tissue with ProteinChip arrays - a way to new insights into carcinogenesis and to ***diagnostic*** tools
AU Wellmann, Axel; Wollscheid, Volker; Lu, Hong; Ma, Zhan Lu; Albers, Peter; Schutze, Karin; Rohde, Volker; Behrens, Peter; Dreschers, Stefan; Ko, Yon; Wernert, Nicolas
CS Institute of Pathology, University of Bonn, Bonn, D-53127, Germany
SO International Journal of Molecular Medicine (2002), 9(4), 341-347
CODEN: IJMMFG; ISSN: 1107-3756
PB International Journal of Molecular Medicine
DT Journal
LA English
CC 9-5 (Biochemical Methods)
Section cross-reference(s): 14
AB Prostate carcinomas are one of the most common malignancies in western societies. The pathogenesis of this tumor is still poorly understood. These tumors present with two characteristic features: epithelial-mesenchymal interactions, which play a pivotal role for tumor development and most of clin. manifest cancers arise in prostate proper compared to a minority of tumors which develop in the transitional zone. Deciphering the epithelial-mesenchymal cross talk and identification of mol. pecularities of the sub-populations of cells in different zones can therefore help understanding carcinogenesis and development of new, non-invasive tools for the diagnosis and prognosis of prostate carcinomas which has remained a challenge until today. A ProteinChip array technol. (SELDI = ***surface*** ***enhanced*** ***laser*** ***desorption*** ***ionization***) has been developed recently by Ciphergen Biosystems enabling anal. and profiling of complex protein mixts. from a few cells. This study describes the anal. of approx. 500-1000 freshly obtained prostate cells by SELDI-TOF-MS (***surface*** ***enhanced*** ***laser*** ***desorption*** ***ionization*** time-of-flight mass spectrometry). Pure cell populations of stroma, epithelium and tumor cells were selected by laser assisted microdissection. Multiple specific protein patterns were reproducibly detected in the range from 1.5 to 30 kDa in 28 sub-populations of 4 tumorous prostates and 1 control. A specific 4.3 kDa peak was increased in the prostate tumor stroma compared to normal prostate proper and transitional zone stroma and increased in prostate tumor glands compared to normal prostate proper and transitional zone glands. Coupling laser assisted microdissection with SELDI provides tremendous opportunities to identify cell and tumor specific proteins to understand mol. events underlying prostate carcinoma development. It underlines the vast potential of this technol. to better understand pathogenesis and identify potential candidates for new specific biomarkers in general which could help to screen for and distinguish disease entities, i.e. between clin. significant and insignificant carcinomas of the prostate.
ST prostate cancer tissue protein chip array SELDI TOF
IT Time-of-flight mass spectrometry

arrays as a way to new insights into carcinogenesis and to ***diagnostic*** tools)
IT Diagnosis
(agents; anal. of microdissected prostate tissue with ProteinChip arrays as a way to new insights into carcinogenesis and to ***diagnostic*** tools)
IT Animal tissue
Prostate gland, neoplasm
Protein microarray technology
Transformation, neoplastic
(anal. of microdissected prostate tissue with ProteinChip arrays as a way to new insights into carcinogenesis and to ***diagnostic*** tools)
IT Laser cutting
(laser assisted microdissection; anal. of microdissected prostate tissue with ProteinChip arrays as a way to new insights into carcinogenesis and to ***diagnostic*** tools)
IT Laser ionization mass spectrometry
(photodesorption, surface-enhanced, SELDI-TOF; anal. of microdissected prostate tissue with ProteinChip arrays as a way to new insights into carcinogenesis and to ***diagnostic*** tools)
IT Laser desorption mass spectrometry
(photoionization, surface-enhanced, SELDI-TOF; anal. of microdissected prostate tissue with ProteinChip arrays as a way to new insights into carcinogenesis and to ***diagnostic*** tools)
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L3 ANSWER 9 OF 20 CA COPYRIGHT 2004 ACS on STN
AN 138:20712 CA
ED Entered STN: 09 Jan 2003
TI Application of ***surface*** - ***enhanced*** ***laser*** ***desorption*** / ***ionization*** technology to the detection and identification of urinary parvalbumin-.alpha.: A biomarker of compound-induced skeletal muscle toxicity in the rat
AU Dare, Theo O.; Davies, Huw A.; Turton, John A.; Lomas, Lee; Williams, Thomas C.; York, Malcom J.
CS Clinical Pathology, Cellular and Biochemical Toxicology, Safety Assessment, GlaxoSmithKline Research and Development, Hertfordshire, SG12 0DP, UK
SO Electrophoresis (2002), 23(18), 3241-3251
CODEN: ELCTDN; ISSN: 0173-0835
PB Wiley-VCH Verlag GmbH & Co. KGaA
DT Journal
LA English
CC 4-3 (Toxicology)
Section cross-reference(s): 9
AB In toxicity studies, compd.-induced changes are typically evaluated using a combination of endpoints and there are often a no. of potential markers in biol. fluids which can indicate toxic change in tissues and organs. However, some biomarkers are not specific to the organ of injury and therefore there is a continuing search for more sensitive and specific indicators of target organ toxicity. In expts. to assess the potential ***diagnostic*** usefulness of ***surface*** - ***enhanced*** ***laser*** ***desorption*** / ***ionization*** (SELDI) ProteinChip technol., skeletal muscle toxicity was induced in Wistar Han rats by administering 2,3,5,6-tetramethyl-p-phenylenediamine (TMPD). The skeletal muscle toxicity was monitored using established endpoints such as

histopathol., and also using SELDI retentate chromatog. mass spectrometry of urine samples. Clear differences in urinary protein patterns between control and TMPD-treated animals were obsd. on the ProteinChip surfaces. Addnl. a specific urine marker protein of 11.8 kDa was identified in TMPD-dosed rats, and the detection of the marker was related to the degree of skeletal muscle toxicity assessed by recognized clin. pathol. endpoints. The 11.8 kDa protein was identified as parvalbumin-.alpha.. These expts. demonstrated the potential of urinary parvalbumin-.alpha. as a specific, noninvasive, and easily detectable biomarker for skeletal muscle toxicity in the rat and the potential of SELDI technol. for biomarker detection and identification in toxicol. studies.

ST SELDI parvalbumin alpha biomarker skeletal muscle toxicity

IT Biomarkers (biological responses)
Blood analysis
Muscle
Urine analysis
(application of ***surface*** - ***enhanced*** ***laser*** ***desorption*** / ***ionization*** technol. to the detection and identification of urinary parvalbumin-.alpha.-biomarker of compd.-induced skeletal muscle toxicity in rat)

IT Enzymes, biological studies
RL: ANT (Analyte); BSU (Biological study, unclassified); ANST (Analytical study); BIOL (Biological study)
(application of ***surface*** - ***enhanced*** ***laser*** ***desorption*** / ***ionization*** technol. to the detection and identification of urinary parvalbumin-.alpha.-biomarker of compd.-induced skeletal muscle toxicity in rat)

IT Laser ionization mass spectrometry
(photodesorption, surface-enhanced; application of ***surface*** - ***enhanced*** ***laser*** ***desorption*** / ***ionization*** technol. to the detection and identification of urinary parvalbumin-.alpha.-biomarker of compd.-induced skeletal muscle toxicity in rat)

IT Laser desorption mass spectrometry
(photoionization, surface-enhanced; application of ***surface*** - ***enhanced*** ***laser*** ***desorption*** / ***ionization*** technol. to the detection and identification of urinary parvalbumin-.alpha.-biomarker of compd.-induced skeletal muscle toxicity in rat)

IT Parvalbumins
RL: ANT (Analyte); BUU (Biological use, unclassified); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(.alpha.-; application of ***surface*** - ***enhanced*** ***laser*** ***desorption*** / ***ionization*** technol. to the detection and identification of urinary parvalbumin-.alpha.-biomarker of compd.-induced skeletal muscle toxicity in rat)

IT 3102-87-2, 2,3,5,6-Tetramethyl-p-phenylenediamine
RL: ADV (Adverse effect, including toxicity); BIOL (Biological study)
(application of ***surface*** - ***enhanced*** ***laser*** ***desorption*** / ***ionization*** technol. to the detection and identification of urinary parvalbumin-.alpha.-biomarker of compd.-induced skeletal muscle toxicity in rat)

IT 9000-86-6, Alanine aminotransferase 9000-97-9, Aspartate aminotransferase 9001-15-4, Creatine kinase 9001-46-1, Glutamate dehydrogenase 9024-52-6, Aldolase
RL: ANT (Analyte); BSU (Biological study, unclassified); ANST (Analytical study); BIOL (Biological study)
(application of ***surface*** - ***enhanced*** ***laser*** ***desorption*** / ***ionization*** technol. to the detection and identification of urinary parvalbumin-.alpha.-biomarker of compd.-induced skeletal muscle toxicity in rat)

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AN 137:383041 CA
ED Entered STN: 19 Dec 2002
TI Normal, benign, preneoplastic, and malignant prostate cells have distinct protein expression profiles resolved by ***surface*** ***enhanced*** ***laser*** ***desorption*** / ***ionization*** mass spectrometry
AU Cazares, Lisa H.; Adam, Bao-Ling; Ward, Michael D.; Nasim, Suhail; Schellhammer, Paul F.; Semmes, O. John; Wright, George L., Jr.
CS Departments of Microbiology and Molecular Cell Biology, Eastern Virginia Medical School and Sentara Cancer Institute, Norfolk, VA, 23501, USA
SO Clinical Cancer Research (2002), 8(8), 2541-2552
CODEN: CCREF4; ISSN: 1078-0432
PB American Association for Cancer Research
DT Journal
LA English
CC 14-1 (Mammalian Pathological Biochemistry)
AB Purpose: The objective of this study was to discover protein biomarkers that differentiate malignant from non-malignant cell populations, esp. early protein alterations that signal the initiation of a developing cancer. The authors hypothesized that ***Surface*** ***Enhanced*** ***Laser*** ***Desorption*** / ***Ionization*** -time of flight-mass spectrometry-assisted protein profiling could detect these protein alterations. Exptl. Design: Epithelial cell populations [benign prostatic hyperplasia (BPH), prostate intraepithelial neoplasia (PIN), and prostate cancer (PCA)] were procured from nine prostatectomy specimens using laser capture microdissection. ***Surface*** ***Enhanced*** ***Laser*** ***Desorption*** / ***Ionization*** -time of flight-mass spectrometry anal. was performed on cell lysates, and the relative intensity levels of each protein or peptide in the mass spectra was calcd. and compared for each cell type. Results: Several small mol. mass peptides or proteins (3000-5000 Da) were found in greater abundance in PIN and PCA cell lysates. Another peak, with an av. mass of 5666 Da, was obsd. to be up-regulated in 86% of the BPH cell lysates. Higher levels of this same peak were found in only 22% of the PIN lysates and none of the PCA lysates. Expression differences were also found for intracellular levels of prostate-specific antigen, which were reduced in PIN and PCA cells when compared with matched normals. Although no single protein alteration was obsd. in all PIN/PCA samples, combining two or more of the markers was effective in distinguishing the benign cell types (normal/BPH) from diseased cell types (PIN/PCA). Logistic regression anal. using seven differentially expressed proteins resulted in a predictive equation that correctly distinguished the diseased lysates with a sensitivity and specificity of 93.3 and 93.8%, resp. Conclusions: We have shown that the protein profiles from prostate cells with different disease states have discriminating differences. These differentially regulated proteins are potential markers for early detection and/or risk factors for development of prostate cancer. Studies are under way to identify these protein/peptides, with the goal of developing a ***diagnostic*** test for the early detection of prostate cancer.
ST protein expression profile prostate hyperplasia cancer
IT Prostate gland, disease
(benign hyperplasia; normal, benign, preneoplastic, and malignant prostate cells have distinct protein expression profiles resolved by ***surface*** ***enhanced*** ***laser*** ***desorption*** / ***ionization*** mass spectrometry)
IT Diagnosis
(cancer; normal, benign, preneoplastic, and malignant prostate cells have distinct protein expression profiles resolved by ***surface*** ***enhanced*** ***laser*** ***desorption*** / ***ionization*** mass spectrometry)
IT Human
Prostate gland, neoplasm
Tumor markers
(normal, benign, preneoplastic, and malignant prostate cells have distinct protein expression profiles resolved by ***surface*** ***enhanced*** ***laser*** ***desorption*** / ***ionization*** mass spectrometry)
IT Prostate-specific antigen
Proteins
Proteome
RL: BSU (Biological study, unclassified); DGN (Diagnostic use); BIOL (Biological study); USES (Uses)
(normal, benign, preneoplastic, and malignant prostate cells have distinct protein expression profiles resolved by ***surface*** ***enhanced*** ***laser*** ***desorption*** / ***ionization*** mass spectrometry)
RE.CNT 40 THERE ARE 40 CITED REFERENCES AVAILABLE FOR THIS RECORD

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L3 ANSWER 11 OF 20 CA COPYRIGHT 2004 ACS on STN
AN 137:275377 CA
ED Entered STN: 31 Oct 2002
TI Method for correlating gene expression profiles with protein expression profiles
IN Rich, William E.; Hutchens, T. William
PA Ciphergen Biosystems, Inc., USA
SO PCT Int. Appl., 58 pp.
CODEN: PIXXD2
DT Patent
LA English
IC ICM C12Q
CC 9-16 (Biochemical Methods)
Section cross-reference(s): 3
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 2002079491	A2	20021010	WO 2002-US4467	20020215
W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
RW:	GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG			
US 2003054367	A1	20030320	US 2002-76967	20020215

PRAI US 2001-269772P P 20010216

AB The present invention provides methods for correlating gene expression with protein expression. The methods involve performing gene expression profiling on a sample, selecting one or more expressed genes for further study, detg. a physiochem. property characteristic of the proteins encoded by these genes, and detg. whether the proteins are expressed in the sample using the physiochem. property as an identifier in a protein expression

fractionated using mass spectrometry. In another preferred embodiment, the proteins are fractionated using SELDI (***surface*** ***enhanced*** ***laser*** ***desorption*** ***ionization***). The methods of the invention are therefore useful in the identification of target proteins for drug discovery, and for the identification of ***diagnostic*** markers. The methods of the present invention are also useful for investigating the expression products of different alleles, for, e.g., pharmacogenetic applications. The methods of the present invention are also useful for toxicol. studies, and for investigating the effects of exposure of a cell to varying environmental conditions, such as radiation, e.g., UV radiation, heat, and cold.

ST correlating gene expression profile protein SELDI mass spectrometry

IT Toxicology
(applications to; method for correlating gene expression profiles with protein expression profiles)

IT Glycosylation
(biol., identifying proteins based on; method for correlating gene expression profiles with protein expression profiles)

IT Human
Neoplasm
(cell, gene expression profile of; method for correlating gene expression profiles with protein expression profiles)

IT Temperature effects, biological
(cold, on protein expression; method for correlating gene expression profiles with protein expression profiles)

IT UV radiation
(exposure of a cell to, effect of; method for correlating gene expression profiles with protein expression profiles)

IT Temperature effects, biological
(heat, on protein expression; method for correlating gene expression profiles with protein expression profiles)

IT Electric charge
Epitopes
Hydrophilicity
Hydrophobicity
Isoelectric point
Molecular weight
Physical properties
Protein sequences
(identifying proteins based on; method for correlating gene expression profiles with protein expression profiles)

IT DNA microarray technology
Gene expression profiles
Gene expression profiles, animal
Microarray technology
(method for correlating gene expression profiles with protein expression profiles)

IT Proteins
RL: ANT (Analyte); BSU (Biological study, unclassified); ANST (Analytical study); BIOL (Biological study)
(method for correlating gene expression profiles with protein expression profiles)

IT EST (expressed sequence tag)
mRNA
RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses)
(microarray; method for correlating gene expression profiles with protein expression profiles)

IT Genetics
(pharmacogenetics, applications to; method for correlating gene expression profiles with protein expression profiles)

IT Laser ionization mass spectrometry
(photodesorption, surface-enhanced, use in protein identification; method for correlating gene expression profiles with protein expression profiles)

IT Laser desorption mass spectrometry
(photoionization, surface-enhanced, use in protein identification; method for correlating gene expression profiles with protein expression profiles)

IT Dyes
(protein binding to; method for correlating gene expression profiles with protein expression profiles)

IT Antibodies
Chelates
Ligands
RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses)

with protein expression profiles)
IT Phosphorylation, biological
(protein, identifying proteins based on; method for correlating gene expression profiles with protein expression profiles)
IT Gel electrophoresis
(two-dimensional, use in protein identification; method for correlating gene expression profiles with protein expression profiles)
IT Chromatography
Mass spectrometry
Protein degradation
(use in protein identification; method for correlating gene expression profiles with protein expression profiles)

L3 ANSWER 12 OF 20 CA COPYRIGHT 2004 ACS on STN
AN 137:259585 CA
ED Entered STN: 24 Oct 2002
TI Proteomics and bioinformatics approaches for identification of serum biomarkers to detect breast cancer
AU Li, Jinong; Zhang, Zhen; Rosenzweig, Jason; Wang, Young Y.; Chan, Daniel W.
CS Department of Pathology, Johns Hopkins Medical Institutions, Baltimore, MD, 21287, USA
SO Clinical Chemistry (Washington, DC, United States) (2002), 48(8), 1296-1304
CODEN: CLCHAU; ISSN: 0009-9147
PB American Association for Clinical Chemistry
DT Journal
LA English
CC 9-16 (Biochemical Methods)
Section cross-reference(s): 14
AB Background: ***Surface*** - ***enhanced*** ***laser*** ***desorption*** / ***ionization*** (SELDI) is an affinity-based mass spectrometric method in which proteins of interest are selectively adsorbed to a chem. modified surface on a biochip, whereas impurities are removed by washing with buffer. This technol. allows sensitive and high-throughput protein profiling of complex biol. specimens. Methods: We screened for potential tumor biomarkers in 169 serum samples, including samples from a cancer group of 103 breast cancer patients at different clin. stages [stage 0 (n = 4), stage I (n = 38), stage II (n = 37), and stage III (n = 24)], from a control group of 41 healthy women, and from 25 patients with benign breast diseases. Dild. serum samples were applied to immobilized metal affinity capture Ciphergen Protein Chip Arrays previously activated with Ni2+. Proteins bound to the chelated metal were analyzed on a ProteinChip Reader Model PBS II. Complex protein profiles of different ***diagnostic*** groups were compared and analyzed using the Pro Peak software package. Results: A panel of three biomarkers was selected based on their collective contribution to the optimal sepn. between stage 0-I breast cancer patients and non-cancer controls. The same sepn. was obsd. using independent test data from stage II-III breast cancer patients. Bootstrap cross-validation demonstrated that a sensitivity of 93% for all cancer patients and a specificity of 91% for all controls were achieved by a composite index derived by multivariate logistic regression using the three selected biomarkers. Conclusions: Proteomics approaches such as SELDI mass spectrometry, in conjunction with bioinformatics tools, could greatly facilitate the discovery of new and better biomarkers. The high sensitivity and specificity achieved by the combined use of the selected biomarkers show great potential for the early detection of breast cancer.
ST proteome bioinformatic serum biomarker detect breast cancer
IT Laser ionization mass spectrometry
(photodesorption, surface-enhanced; proteomics and bioinformatics approaches for identification of serum biomarkers to detect breast cancer)
IT Laser desorption mass spectrometry
(photoionization, surface-enhanced; proteomics and bioinformatics approaches for identification of serum biomarkers to detect breast cancer)
IT Bioinformatics
Biomarkers (biological responses)
Blood serum
High throughput screening
Human
Mammary gland, neoplasm
Simulation and Modeling, biological
Statistical analysis
(proteomics and bioinformatics approaches for identification of serum

IT Proteins
RL: ANT (Analyte); BSU (Biological study, unclassified); DGN (Diagnostic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(proteomics and bioinformatics approaches for identification of serum biomarkers to detect breast cancer)

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L3 ANSWER 13 OF 20 CA COPYRIGHT 2004 ACS on STN
AN 137:199271 CA
ED Entered STN: 26 Sep 2002
TI Serum protein fingerprinting coupled with a pattern-matching algorithm distinguishes prostate cancer from benign prostate hyperplasia and healthy men
AU Adam, Bao-Ling; Qu, Yinsheng; Davis, John W.; Ward, Michael D.; Clements, Mary Ann; Cazares, Lisa H.; Semmes, O. John; Schellhammer, Paul F.; Yasui, Yutaka; Feng, Ziding; Wright, George L., Jr.
CS Departments of Microbiology and Molecular Cell Biology, Virginia Prostate Center, Eastern Virginia Medical School, Norfolk, VA, 23501, USA
SO Cancer Research (2002), 62(13), 3609-3614
CODEN: CNREA8; ISSN: 0008-5472
PB American Association for Cancer Research
DT Journal
LA English
CC 14-1 (Mammalian Pathological Biochemistry)
Section cross-reference(s): 3
AB The prostate-specific antigen test has been a major factor in increasing awareness and better patient management of prostate cancer (PCA), but its lack of specificity limits its use in diagnosis and makes for poor early detection of PCA. The objective of our studies is to identify better biomarkers for early detection of PCA using protein profiling technologies that can simultaneously resolve and analyze multiple proteins. Evaluating multiple proteins will be essential to establishing signature proteomic patterns that distinguish cancer from noncancer as well as identify all genetic subtypes of the cancer and their biol. activity. In this study, we used a protein biochip ***surface*** ***enhanced*** ***laser*** ***desorption*** / ***ionization*** mass spectrometry approach coupled with an artificial intelligence learning algorithm to differentiate PCA from noncancer cohorts. ***Surface*** ***enhanced*** ***laser*** ***desorption*** / ***ionization*** mass spectrometry protein profiles of serum from 167 PCA patients, 77 patients with benign prostate hyperplasia, and 82 age-matched unaffected healthy men were used to train and develop a decision tree classification algorithm that used a nine-protein mass pattern that correctly classified 96% of the samples. A blinded test set, sepd. from the training set by a stratified random sampling before the anal., was used to det. the sensitivity and specificity of the classification system. A sensitivity of 83%, a specificity of 97%, and a pos. predictive value of 96% for the study population and 91% for the general population were obtained when comparing the PCA vs. non-cancer (benign prostate hyperplasia/healthy men) groups. This high-throughput proteomic classification system will provide a highly accurate and innovative approach for the early detection/diagnosis of PCA.
ST protein fingerprinting PSA diagnosis prostate cancer hyperplasia
IT Prostate gland, disease
(benign hyperplasia; serum protein fingerprinting and prostate-specific antigen as early ***diagnostic*** and prognostic markers for prostate cancer and benign prostate hyperplasia in men)

RL: BSU (Biological study, unclassified); DGN (Diagnostic use); BIOL (Biological study); USES (Uses)
(blood, fingerprinting; serum protein fingerprinting and prostate-specific antigen as early ***diagnostic*** and prognostic markers for prostate cancer and benign prostate hyperplasia in men)
IT Diagnosis
(cancer; serum protein fingerprinting and prostate-specific antigen as early ***diagnostic*** and prognostic markers for prostate cancer and benign prostate hyperplasia in men)
IT Prostate gland, neoplasm
(carcinoma; serum protein fingerprinting and prostate-specific antigen as early ***diagnostic*** and prognostic markers for prostate cancer and benign prostate hyperplasia in men)
IT Diagnosis
(genetic; serum protein fingerprinting and prostate-specific antigen as early ***diagnostic*** and prognostic markers for prostate cancer and benign prostate hyperplasia in men)
IT Aging, animal
Biomarkers (biological responses)
DNA fingerprinting
Human
Prognosis
(serum protein fingerprinting and prostate-specific antigen as early ***diagnostic*** and prognostic markers for prostate cancer and benign prostate hyperplasia in men)
IT Prostate-specific antigen
RL: BSU (Biological study, unclassified); DGN (Diagnostic use); BIOL (Biological study); USES (Uses)
(serum protein fingerprinting and prostate-specific antigen as early ***diagnostic*** and prognostic markers for prostate cancer and benign prostate hyperplasia in men)
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L3 ANSWER 14 OF 20 CA COPYRIGHT 2004 ACS on STN
AN 136:383614 CA
ED Entered STN: 13 Jun 2002
TI Cancer proteomics: New developments in clinical chemistry

AU Rai, A. J.; Chan, D. W.
CS Dept. of Pathology, Div. of Clinical Chemistry, The Johns Hopkins University School of Medicine, Baltimore, MD, 21287, USA

SO Laboratoriumsmedizin (2001), 25(9-10), 399-403
CODEN: LABOD3; ISSN: 0342-3026
PB Blackwell Wissenschafts-Verlag GmbH
DT Journal; General Review
LA English

CC 14-0 (Mammalian Pathological Biochemistry)

AB A review. The entire protein complement of a cell is termed the proteome. "Proteomics" is defined as the systematic expression of diverse properties of proteins in a cell. Proteomic methodologies can detect protein modifications, which occur after protein synthesis. The anal. of the proteome thus provides useful information, which can be used for the identification and screening of ***diagnostic*** markers, and is relevant for the understanding of tumor-progression. In past years, the most widely used tool of proteome-anal. was 2D-gel electrophoresis. Today, new methods are available, which are based on biochip technol.

protein matrixes and specify functional aspects of tumor-progression. After initial isolation, the sepd. proteins are identified by mass spectrometry based techniques such as MALDI (matrix assisted laser desorption ionization) or SELDI (***surface*** ***enhanced*** ***laser*** ***desorption*** ***ionization***) - TOF (time of flight). This review focuses on new developments in proteomics, including SELDI, and describes applications of these methods for the search of new "protein signatures" in cancer research. It is expected that the advancements of proteomics-techniques will help to classify human cancer by mol. rather than morphol. characteristics.

ST review human cancer marker proteome

IT DNA microarray technology
Human
Mass spectrometry
Neoplasm
Tumor markers
(cancer proteomics, new developments in clin. chem.)

IT Proteome
RL: ADV (Adverse effect, including toxicity); DGN (Diagnostic use); PRP (Properties); BIOL (Biological study); USES (Uses)
(cancer proteomics, new developments in clin. chem.)

RE.CNT 9 THERE ARE 9 CITED REFERENCES AVAILABLE FOR THIS RECORD

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L3 ANSWER 15 OF 20 CA COPYRIGHT 2004 ACS on STN

AN 136:365982 CA

ED Entered STN: 06 Jun 2002

TI An integrated approach utilizing artificial neural networks and SELDI mass spectrometry for the classification of human tumors and rapid identification of potential biomarkers

AU Ball, G.; Mian, S.; Holding, F.; Allibone, R. O.; Lowe, J.; Ali, S.; Li, G.; McCardle, S.; Ellis, I. O.; Creaser, C.; Rees, R. C.

CS Department of Life Sciences, Nottingham Trent University, Nottingham, NG11 8NS, UK

SO Bioinformatics (2002), 18(3), 395-404
CODEN: BOINFP; ISSN: 1367-4803

PB Oxford University Press

DT Journal

LA English

CC 9-5 (Biochemical Methods)
Section cross-reference(s): 14

AB Motivation: MALDI mass spectrometry is able to elicit macromol. expression data from cellular material and when used in conjunction with Ciphergen protein chip technol. (also referred to as SELDI- ***Surface*** ***Enhanced*** ***Laser*** ***Desorption*** / ***Ionization***), it permits a semi-high throughput approach to be taken with respect to sample processing and data acquisition. Due to the large array of data that is generated from a single anal. (8-10 000 variables using a mass range of 2-15 kDa-this paper) it is essential to implement the use of algorithms that can detect expression patterns from such large vols. of data correlating to a given biol./pathol. phenotype from multiple samples. If successful, the methodol. could be extrapolated to larger data sets to enable the identification of validated biomarkers correlating strongly to disease progression. This would not only serve to enable tumors to be classified according to their mol. expression profile but could also focus attention upon a relatively small no. of mols. that might warrant further biochem./mol. characterization to assess their suitability as potential therapeutic targets. Results: Using a multi-layer perceptron Artificial Neural Network (ANN) (Neuroshell 2) with a back propagation algorithm we have developed a prototype approach that uses a model system (comprising five low and seven high-grade human astrocytomas) to identify mass spectral peaks whose relative intensity values correlate strongly to tumor grade. Analyzing data derived from MALDI mass spectrometry in conjunction with Ciphergen protein chip technol. we have used relative importance values, detd. from the wts. of trained ANNs, to identify masses that accurately predict tumor grade. Implementing a three-stage procedure, we have screened a population of approx. 100 000-120 000 variables and

intensity pattern was significantly reduced in high-grade astrocytoma. The data from this initial study suggests that application of ANN-based approaches can identify mol. ion patterns which strongly assoc. with disease grade and that its application to larger cohorts of patient material could potentially facilitate the rapid identification of validated biomarkers having significant clin. (i.e. ***diagnostic*** /prognostic) potential for the field of cancer biol.

ST artificial neural network SELDI mass spectrometry tumor biomarker

IT Diagnosis
(agents; integrated approach utilizing artificial neural networks and SELDI mass spectrometry for classification of human tumors and rapid identification of potential biomarkers)

IT Algorithm
Animal tissue
Biomarkers (biological responses)
Computer program
Human
Microarray technology
Neoplasm
Sample preparation
(integrated approach utilizing artificial neural networks and SELDI mass spectrometry for classification of human tumors and rapid identification of potential biomarkers)

IT Proteins
RL: ANT (Analyte); DGN (Diagnostic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(integrated approach utilizing artificial neural networks and SELDI mass spectrometry for classification of human tumors and rapid identification of potential biomarkers)

IT Astrocyte
(neoplasm, astrocytoma; integrated approach utilizing artificial neural networks and SELDI mass spectrometry for classification of human tumors and rapid identification of potential biomarkers)

IT Simulation and Modeling, physicochemical
(neural network; integrated approach utilizing artificial neural networks and SELDI mass spectrometry for classification of human tumors and rapid identification of potential biomarkers)

IT Laser ionization mass spectrometry
(photodesorption, matrix-assisted; integrated approach utilizing artificial neural networks and SELDI mass spectrometry for classification of human tumors and rapid identification of potential biomarkers)

IT Laser ionization mass spectrometry
(photodesorption, surface-enhanced; integrated approach utilizing artificial neural networks and SELDI mass spectrometry for classification of human tumors and rapid identification of potential biomarkers)

IT Laser desorption mass spectrometry
(photoionization, matrix-assisted; integrated approach utilizing artificial neural networks and SELDI mass spectrometry for classification of human tumors and rapid identification of potential biomarkers)

IT Laser desorption mass spectrometry
(photoionization, surface-enhanced; integrated approach utilizing artificial neural networks and SELDI mass spectrometry for classification of human tumors and rapid identification of potential biomarkers)

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L3 ANSWER 16 OF 20 CA COPYRIGHT 2004 ACS on STN
AN 136:365893 CA
ED Entered STN: 06 Jun 2002
TI The SELDI-TOF MS approach to proteomics: Protein profiling and biomarker identification
AU Issaq, Haleem J.; Veenstra, Timothy D.; Conrads, Thomas P.; Felschow, Donna
CS SAIC-Frederick, Inc., National Cancer Institute at Frederick, Frederick, MD, 21702, USA
SO Biochemical and Biophysical Research Communications (2002), 292(3), 587-592
CODEN: BBRCA9; ISSN: 0006-291X
PB Elsevier Science
DT Journal; General Review
LA English
CC 9-0 (Biochemical Methods)
AB A review. The need for methods to identify disease biomarkers is underscored by the survival-rate of patients diagnosed at early stages of cancer progression. ***surface*** ***enhanced*** ***laser*** ***desorption*** / ***ionization*** time-of-flight mass spectrometry (SELDI-TOF MS) is a novel approach to biomarker discovery that combines two powerful techniques: chromatog. and mass spectrometry. One of the key features of SELDI-TOF MS is its ability to provide a rapid protein expression profile from a variety of biol. and clin. samples. It has been used for biomarker identification as well as the study of protein-protein, and protein-DNA interaction. The versatility of SELDI-TOF MS has allowed its use in projects ranging from the identification of potential ***diagnostic*** markers for prostate, bladder, breast, and ovarian cancers and Alzheimer's disease, to the study of biomol. interactions and the characterization of post-translational modifications. In this minireview we discuss the application of SELDI-TOF MS to protein biomarker discovery and profiling.
ST review SELDI TOF MS protein profiling biomarker
IT Biomarkers (biological responses)
Neoplasm
Time-of-flight mass spectrometry
(SELDI-TOF MS approach to proteomics)
IT Proteins
RL: ANT (Analyte); DGN (Diagnostic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(SELDI-TOF MS approach to proteomics)
IT Diagnosis
(agents; SELDI-TOF MS approach to proteomics)
IT Laser ionization mass spectrometry
(photodesorption, surface-enhanced; SELDI-TOF MS approach to proteomics)
IT Laser desorption mass spectrometry
(photoionization, surface-enhanced; SELDI-TOF MS approach to proteomics)
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L3 ANSWER 17 OF 20 CA COPYRIGHT 2004 ACS on STN
AN 136:34118 CA
ED Entered STN: 10 Jan 2002
TI Development of a novel proteomic approach for the detection of transitional cell carcinoma of the bladder in urine
AU Vlahou, Antonia; Schellhammer, Paul F.; Mendrinos, Savvas; Patel, Keyur; Kondylis, Filippos I.; Gong, Lei; Nasim, Suhail; Wright, George L., Jr.
CS Departments of Microbiology and Molecular Cell Biology, Eastern Virginia Medical School, Norfolk, VA, 23507, USA
SO American Journal of Pathology (2001), 158(4), 1491-1502
CODEN: AJPAA4; ISSN: 0002-9440
PB American Society for Investigative Pathology
DT Journal
LA English
CC 9-5 (Biochemical Methods)
Section cross-reference(s): 14
AB Development of noninvasive methods for the diagnosis of transitional cell carcinoma (TCC) of the bladder remains a challenge. A ProteinChip technol. (***surface*** ***enhanced*** ***laser*** ***desorption*** / ***ionization*** time of flight mass spectrometry) has recently been developed to facilitate protein profiling of biol. mixts. This report describes an exploratory study of this technol. as a TCC ***diagnostic*** tool. Ninety-four urine samples from patients with TCC, patients with other urogenital diseases, and healthy donors were analyzed. Multiple protein changes were reproducibly detected in the TCC group, including five potential novel TCC biomarkers and seven protein clusters (mass range, 3.3 to 133 kDa). One of the TCC biomarkers (3.4 kDa) was also detected in bladder cancer cells procured from bladder barbotage and was identified as defensin. The TCC detection rates provided by the individual markers ranged from 43 to 70% and specificities from 70 to 86%. Combination of the protein biomarkers and clusters, increased significantly the sensitivity for detecting TCC to 87% with a specificity of 66%. Interestingly, this combinatorial approach provided sensitivity of 78% for detecting low-grade TCC compared to only 33% of voided urine or bladder-washing cytol. Collectively these results support the potential of this proteomic approach for the development of a highly sensitive urinary TCC ***diagnostic*** test.
ST development proteomic detection transitional cell carcinoma bladder urine
IT Diagnosis
(cancer; development of a novel proteomic approach for detection of transitional cell carcinoma of bladder in urine)
IT Animal cell
Tumor markers
Urine analysis
(development of a novel proteomic approach for detection of transitional cell carcinoma of bladder in urine)
IT Proteins
Proteome
RL: ANT (Analyte); DGN (Diagnostic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(development of a novel proteomic approach for detection of transitional cell carcinoma of bladder in urine)
IT Urogenital tract
(disease; development of a novel proteomic approach for detection of transitional cell carcinoma of bladder in urine)
IT Time-of-flight mass spectrometry
(***surface*** ***enhanced*** ***laser*** ***desorption*** / ***ionization*** ; development of a novel proteomic approach for detection of transitional cell carcinoma of bladder in urine)
IT Bladder, neoplasm
(transitional cell carcinoma; development of a novel proteomic approach for detection of transitional cell carcinoma of bladder in urine)
IT 103220-14-0, Defensin
RL: ANT (Analyte); DGN (Diagnostic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(development of a novel proteomic approach for detection of transitional cell carcinoma of bladder in urine)
RE.CNT 46 THERE ARE 46 CITED REFERENCES AVAILABLE FOR THIS RECORD
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L3 ANSWER 18 OF 20 CA COPYRIGHT 2004 ACS on STN
AN 135:368779 CA
ED Entered STN: 13 Dec 2001
TI Toward proteomics in uroscopy: Urinary protein profiles after radiocontrast medium administration
AU Hampel, Dierk J.; Sansome, Christine; Sha, Ma; Brodsky, Sergey; Lawson, William E.; Goligorsky, Michael S.
CS Departments of Medicine Division of Nephrology and Hypertension, State University of New York at Stony Brook, Stony Brook, NY, T15-020, USA
SO Journal of the American Society of Nephrology (2001), 12(5), 1026-1035
CODEN: JASNEU; ISSN: 1046-6673
PB Lippincott Williams & Wilkins
DT Journal
LA English
CC 9-5 (Biochemical Methods)
Section cross-reference(s): 14
AB Previous attempts to use urinary protein profiles for ***diagnostic*** purposes have been rather disappointing with respect to their clin. validity, in part because of the insufficient reproducibility, sensitivity, and rapidity of available techniques. Therefore, a newly developed, high-throughput technique, namely ***surface*** - ***enhanced*** ***laser*** ***desorption*** / ***ionization*** (SELDI) ProteinChip array-time of flight mass spectrometry, was studied, to assess its applicability for protein profiling of urine and to exemplify its use for a group of patients receiving radiocontrast medium. Assessment of the accuracy, sensitivity, and reproducibility of SELDI in test urinary protein profiling was performed. Renal function was studied in 20 male Sprague-Dawley rats before and after i.v. administration of either 1.25 g/kg ioxilan (n = 10) or hypertonic saline soln. (n = 10) as a control. Urine samples from 25 patients undergoing cardiac catheterization were obtained before, immediately after, and 6 to 12 h after the procedure. Administration of ioxilan to rats resulted in

For patients, even in uncomplicated cases of radiocontrast medium infusion during cardiac catheterization, perturbations in the protein compn. occurred but returned to baseline values after 6 to 12 h. Protein with mol. masses of 9.75, 11.75, 23.5, and 66.4 kDa changed in abundance. For patients with impaired renal function, these changes were not reversible within 6 to 12 h. As a proof of principle, one of the peaks, i.e., that at 11.75 kDa, was identified as .beta.2-microglobulin. SELDI is a promising tool for the detection, identification, and characterization of trace amts. of proteins in urine. Even for patients without renal complications, proteins with a broad range of mol. masses either appear in or disappear from the urine. Some of these might represent markers of impending nephropathy.

ST kidney protein urine array laser mass spectrometry microglobulin

IT Biotechnology
(biochips, ProteinChip array; ***surface*** - ***enhanced*** ***laser*** ***desorption*** / ***ionization*** (SELDI) ProteinChip array-time of flight mass spectrometry for urine protein anal.)

IT Imaging agents
(radio contrasting; ***surface*** - ***enhanced*** ***laser*** ***desorption*** / ***ionization*** (SELDI) ProteinChip array-time of flight mass spectrometry for urine protein anal.)

IT Kidney
Time-of-flight mass spectrometry
Urine analysis
(***surface*** - ***enhanced*** ***laser*** ***desorption*** / ***ionization*** (SELDI) ProteinChip array-time of flight mass spectrometry for urine protein anal.)

IT Proteins, general, analysis
RL: ANT (Analyte); PRP (Properties); ANST (Analytical study)
(***surface*** - ***enhanced*** ***laser*** ***desorption*** / ***ionization*** (SELDI) ProteinChip array-time of flight mass spectrometry for urine protein anal.)

IT Laser desorption mass spectrometry
Laser ionization mass spectrometry
(***surface*** - ***enhanced*** ***laser*** ***desorption*** / ***ionization*** (SELDI) ProteinChip array; ***surface*** - ***enhanced*** ***laser*** ***desorption*** / ***ionization*** (SELDI) ProteinChip array-time of flight mass spectrometry for urine protein anal.)

IT Microglobulins
RL: ANT (Analyte); BPR (Biological process); BSU (Biological study, unclassified); ANST (Analytical study); BIOL (Biological study); PROC (Process)
(.beta.2-; ***surface*** - ***enhanced*** ***laser*** ***desorption*** / ***ionization*** (SELDI) ProteinChip array-time of flight mass spectrometry for urine protein anal.)

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L3 ANSWER 19 OF 20 CA COPYRIGHT 2004 ACS on STN

AN 135:209050 CA

ED Entered STN: 27 Sep 2001

TI Expression and regulation of procalcitonin in different human cells and tissues

AU Russwurm, S.; Stonans, I.; Wiederhold, M.; Meisner, M.; Oberhoffer, M.; Zipfel, P. F.; Reinhart, K.

CS Clinic of Anesthesiology and Critical Care, Friedrich-Schiller-University,

SO Trauma, Shock, Inflammation and Sepsis: Pathophysiology, Immune Consequences and Therapy, World Congress, 5th, Munich, Germany, Feb. 29-Mar. 4, 2000 (2000), 29-33. Editor(s): Faist, Eugen. Publisher: Monduzzi Editore, Bologna, Italy.
CODEN: 69BDIP
DT Conference
LA English
CC 14-3 (Mammalian Pathological Biochemistry)
AB Procalcitonin (PCT), the precursor of calcitonin, was recently forwarded as a ***diagnostic*** marker of systemic bacterial infection and sepsis. The major PCT prodn. site in sepsis still remains unknown. The goal of this study was to analyze various potential human sources of PCT such as different cell types (peripheral blood monocytes, human umbilical venae endothelial cells - HUVEC), cell lines (liver parenchymal cells - HepG2 liver hepatoma) and tissues (liver). PCT mRNA expression was estd. using RT-PCR. The intracellular PCT protein expression was verified by Western blotting and ***surface*** - ***enhanced*** ***laser*** ***desorption*** / ***ionization*** (SELDI). Expression of PCT was detd. in liver tissue and monocytes, but it was absent in liver parenchymal cells and endothelial cells. Therefore, monocytes and liver macrophages (Kupffer cells) may be among the sources of elevated PCT levels in septic patients.
ST sepsis procalcitonin liver Kupffer cell monocyte
IT Liver
(Kupffer cell; procalcitonin expression and regulation in human cells and tissues)
IT Liver
Monocyte
Sepsis
(procalcitonin expression and regulation in human cells and tissues)
IT 56645-65-9, Procalcitonin
RL: BOC (Biological occurrence); BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); OCCU (Occurrence); PROC (Process)
(procalcitonin expression and regulation in human cells and tissues)
RE.CNT 4 THERE ARE 4 CITED REFERENCES AVAILABLE FOR THIS RECORD
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L3 ANSWER 20 OF 20 CA COPYRIGHT 2004 ACS on STN
AN 135:192394 CA
ED Entered STN: 20 Sep 2001
TI Quantitation of serum prostate-specific membrane antigen by a novel protein biochip immunoassay discriminates benign from malignant prostate disease
AU Xiao, Zhen; Adam, Bao-Ling; Cazares, Lisa H.; Clements, Mary Ann; Davis, John W.; Schellhammer, Paul F.; Dalmasso, Enrique A.; Wright, George L., Jr.
CS Department of Microbiology and Molecular Cell Biology and Virginia Prostate Center, Eastern Virginia Medical School, Norfolk, VA, 23507, USA
SO Cancer Research (2001), 61(16), 6029-6033
CODEN: CNREA8; ISSN: 0008-5472
PB American Association for Cancer Research
DT Journal
LA English
CC 9-10 (Biochemical Methods)
Section cross-reference(s): 14
AB The lack of a sensitive immunoassay for quantitating serum prostate-specific membrane antigen (PSMA) hinders its clin. utility as a ***diagnostic*** /prognostic biomarker. An innovative protein biochip immunoassay was used to quantitate and compare serum PSMA levels in healthy men and patients with either benign or malignant prostate disease. PSMA was captured from serum by anti-PSMA antibody bound to ProteinChip arrays, the captured PSMA detected by ***surface*** - ***enhanced*** ***laser*** ***desorption*** / ***ionization*** mass spectrometry, and quantitated by comparing the mass signal integrals to a std. curve established using purified recombinant PSMA. The av. serum PSMA value for prostate cancer (623.1 ng/mL) was significantly different ($P < 0.001$) from that for benign prostate hyperplasia (117.1 ng/mL) and the normal groups (age <50, 272.9 ng/mL; age >50, 359.4 ng/mL). These initial results suggest that serum PSMA may be a more effective biomarker than prostate-specific antigen for differentiating benign from malignant prostate disease and warrants addnl. evaluation of the ***surface*** -

PSMA immunoassay to det. its ***diagnostic*** utility.
ST prostate membrane antigen detn protein biochip immunoassay
IT Diagnosis
(agents; serum prostate-specific membrane antigen detn. by protein biochip immunoassay)
IT Prostate gland
(disease; serum prostate-specific membrane antigen detn. by protein biochip immunoassay)
IT Prostate gland
(neoplasm; serum prostate-specific membrane antigen detn. by protein biochip immunoassay)
IT Biotechnology
Blood serum
Hyperplasia
Immunoassay
(serum prostate-specific membrane antigen detn. by protein biochip immunoassay)
IT Prostate-specific antigen
RL: ANT (Analyte); ANST (Analytical study)
(serum prostate-specific membrane antigen detn. by protein biochip immunoassay)
RE.CNT 22 THERE ARE 22 CITED REFERENCES AVAILABLE FOR THIS RECORD
RE

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=> s matrix(w)assisted(w)laser(w)desorption(w)ionization
389453 MATRIX
56484 ASSISTED
416640 LASER
91306 DESORPTION
227296 IONIZATION
L4 4940 MATRIX(W)ASSISTED(W)LASER(W)DESORPTION(W)IONIZATION

=> s l4 and diagnostic
68256 DIAGNOSTIC
L5 66 L4 AND DIAGNOSTIC

=> s l5 and cationic(w)adsorbent?
107028 CATIONIC
69879 ADSORBENT?
27 CATIONIC(W)ADSORBENT?
L6 0 L5 AND CATIONIC(W)ADSORBENT?

=> s l5 and cationic
107028 CATIONIC
L7 0 L5 AND CATIONIC

=> s l5 and cancer?
201839 CANCER?
L8 11 L5 AND CANCER?

=> d all 1-11

L8 ANSWER 1 OF 11 CA COPYRIGHT 2004 ACS on STN

ED Entered STN: 28 Aug 2003
TI Use of serological proteomic methods to find biomarkers associated with breast ***cancer***
AU Zhao, Rui; Ji, Jian-Guo; Tong, Yuan-Peng; Hai, Pu; Ru, Bing-Gen
CS Laboratory of Proteomics Research, College of Life Sciences, Peking University, Beijing, 100871, Peop. Rep. China
SO Proteomics (2003), 3(4), 433-439
CODEN: PROTC7; ISSN: 1615-9853
PB Wiley-VCH Verlag GmbH & Co. KGaA
DT Journal
LA English
CC 9-5 (Biochemical Methods)
Section cross-reference(s): 14
AB New technologies for the detection and therapy of early stage breast ***cancer*** are urgently needed. Pathol. changes in breast might be reflected in proteomic patterns in serum. A proteomic tool was used to identify proteomic patterns in serum that distinguishes neoplastic from non-neoplastic disease within the breast. Preliminary results derived from the serum anal. from 54 unaffected women and 76 patients with breast ***cancer*** were analyzed by two-dimensional (2-D) electrophoresis and ***matrix*** - ***assisted*** ***laser*** ***desorption*** / ***ionization*** -time of flight mass spectrometry, HSP27 was found up-regulated while 14-3-3 sigma was down-regulated in the serum of breast ***cancer*** patients. The two protein biomarkers were then used to classify an independent set of 104 masked serum samples. The results showed that the protein pattern on 2-D gels can completely segregate the serum of breast ***cancer*** from non- ***cancer*** . The discriminatory pattern correctly identified all 69 breast ***cancer*** cases in the masked set. Of the 35 cases of non-malignant disease, 34 were recognized as non- ***cancer*** . These findings justify a prospective population-based assessment of proteomic technol. as a screening or ***diagnostic*** tool for breast ***cancer*** in high-risk and general populations. These two protein biomarkers could also be used as targets for further study in drug design and breast ***cancer*** therapy.
ST serol proteomic biomarker assocd breast ***cancer***
IT Diagnosis
(agents; use of serol. proteomic methods to find biomarkers assocd. with breast ***cancer***)
IT Laser ionization mass spectrometry
(photodesorption, matrix-assisted; use of serol. proteomic methods to find biomarkers assocd. with breast ***cancer***)
IT Laser desorption mass spectrometry
(photoionization, matrix-assisted; use of serol. proteomic methods to find biomarkers assocd. with breast ***cancer***)
IT Biomarkers (biological responses)
Blood serum
Human
Mammary gland, neoplasm
Time-of-flight mass spectrometry
(use of serol. proteomic methods to find biomarkers assocd. with breast ***cancer***)
IT Proteome
RL: ANT (Analyte); BSU (Biological study, unclassified); DGN (Diagnostic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(use of serol. proteomic methods to find biomarkers assocd. with breast ***cancer***)
RE.CNT 15 THERE ARE 15 CITED REFERENCES AVAILABLE FOR THIS RECORD
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AN 139:63907 CA
ED Entered STN: 24 Jul 2003
TI Analysis and accurate quantification of CpG methylation by MALDI mass spectrometry
AU Tost, Joerg; Schatz, Philipp; Schuster, Matthias; Berlin, Kurt; Gut, Ivo Glynne
CS Centre National de Genotypage, Evry, 91057, Fr.
SO Nucleic Acids Research (2003), 31(9), e50/1-e50/10
CODEN: NARHAD; ISSN: 0305-1048
PB Oxford University Press
DT Journal
LA English
CC 3-1 (Biochemical Genetics)
Section cross-reference(s): 9
AB As the DNA sequence of the human genome is now nearly finished, the main task of genome research is to elucidate gene function and regulation. DNA methylation is of particular importance for gene regulation and is strongly implicated in the development of ***cancer*** . Even minor changes in the degree of methylation can have severe consequences. An accurate quantification of the methylation status at any given position of the genome is a powerful ***diagnostic*** indicator. Here we present the first assay for the anal. and precise quantification of methylation on CpG positions in simplex and multiplex reactions based on ***matrix*** - ***assisted*** ***laser*** ***desorption*** / ***ionization*** mass spectrometry detection. Calibration curves for CpGs in two genes were established and an algorithm was developed to account for systematic fluctuations. Regression anal. gave R2 .gtoreq. 0.99 and std. deviation around 2% for the different positions. The limit of detection was .apprx.5% for the minor isomer. Calibrations showed no significant differences when carried out as simplex or multiplex analyses. All variable parameters were thoroughly investigated, several paraffin-embedded tissue biopsies were analyzed and results were verified by established methods like anal. of cloned material. Mass spectrometric results were also compared to chip hybridization.
ST DNA CpG methylation analysis MALDI mass spectrometry; human GSTP1 FVIII gene tissue sample CpG methylation analysis
IT Genetic element
RL: ANT (Analyte); BUU (Biological use, unclassified); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(CpG island, in FVIII gene; anal. and accurate quantification of CpG methylation by MALDI mass spectrometry using human coagulation factor VIII gene and gene GSTP1)
IT Primers (nucleic acid)
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(DNA, charge tagged; anal. and accurate quantification of CpG methylation by MALDI mass spectrometry)
IT Gene, animal
RL: ANT (Analyte); BUU (Biological use, unclassified); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(GSTP1; anal. and accurate quantification of CpG methylation by MALDI mass spectrometry using human coagulation factor VIII gene and gene GSTP1)
IT Calibration
(anal. and accurate quantification of CpG methylation by MALDI mass spectrometry)
IT Human
(anal. and accurate quantification of CpG methylation by MALDI mass spectrometry using human coagulation factor VIII gene and gene GSTP1)
IT Animal tissue
Prostate gland, neoplasm
(anal. and accurate quantification of CpG methylation by MALDI mass spectrometry using prostate tissue biopsies and gene GSTP1)
IT Deoxyribonucleotides
RL: ARU (Analytical role, unclassified); ANST (Analytical study)
(dideoxyribonucleotides, .alpha.-thio-; anal. and accurate quantification of CpG methylation by MALDI mass spectrometry)
IT Genotyping (method)
(epigenotyping, GOOD assay; anal. and accurate quantification of CpG methylation by MALDI mass spectrometry)
IT Genetic element
RL: ANT (Analyte); BUU (Biological use, unclassified); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(exon, 14 of FVIII gene; anal. and accurate quantification of CpG methylation by MALDI mass spectrometry using human coagulation factor

IT Gene, animal
RL: ANT (Analyte); BUU (Biological use, unclassified); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(for coagulation factor VIII; anal. and accurate quantification of CpG methylation by MALDI mass spectrometry using human coagulation factor VIII gene and gene GSTP1)
IT DNA
RL: ANT (Analyte); BUU (Biological use, unclassified); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(methylation; anal. and accurate quantification of CpG methylation by MALDI mass spectrometry)
IT DNA
RL: ANT (Analyte); BUU (Biological use, unclassified); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(methylcytosine-contg.; anal. and accurate quantification of CpG methylation by MALDI mass spectrometry)
IT Laser ionization mass spectrometry
(photodesorption, matrix-assisted; anal. and accurate quantification of CpG methylation by MALDI mass spectrometry)
IT Laser desorption mass spectrometry
(photoionization, matrix-assisted; anal. and accurate quantification of CpG methylation by MALDI mass spectrometry)
IT DNA
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(primer, charge tagged; anal. and accurate quantification of CpG methylation by MALDI mass spectrometry)
IT 7631-90-5, Sodium bisulfite
RL: ARU (Analytical role, unclassified); RCT (Reactant); ANST (Analytical study); RACT (Reactant or reagent)
(anal. and accurate quantification of CpG methylation by MALDI mass spectrometry)
IT 113189-02-9
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(gene for; anal. and accurate quantification of CpG methylation by MALDI mass spectrometry using human coagulation factor VIII gene and gene GSTP1)
IT 50812-37-8
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(.pi., gene GSTP1; anal. and accurate quantification of CpG methylation by MALDI mass spectrometry using human coagulation factor VIII gene and gene GSTP1)
RE.CNT 24 THERE ARE 24 CITED REFERENCES AVAILABLE FOR THIS RECORD
RE

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L8 ANSWER 3 OF 11 CA COPYRIGHT 2004 ACS on STN
AN 138:399589 CA
ED Entered STN: 19 Jun 2003
TI Protein Expression Profiling Identifies Macrophage Migration Inhibitory Factor and Cyclophilin A as Potential Molecular Targets in Non-Small Cell Lung ***Cancer***

C.; Patz, Edward F.
CS Department of Radiology, Duke University, Durham, NC, 27708, USA
SO Cancer Research (2003), 63(7), 1652-1656
CODEN: CNREA8; ISSN: 0008-5472
PB American Association for Cancer Research
DT Journal
LA English
CC 14-1 (Mammalian Pathological Biochemistry)
Section cross-reference(s): 9, 15
AB Current ***diagnostic*** and therapeutic strategies for lung ***cancer*** have had no significant impact on lung ***cancer*** mortality over the last several decades. This study used a ***matrix*** - ***assisted*** ***laser*** ***desorption*** / ***ionization*** time-of-flight mass spectrometry (MALDI-TOF MS) discovery platform to generate protein expression profiles in search of overexpressed proteins in lung tumors as potentially novel mol. targets. Two differentially expressed protein peaks at m/z 12,338 and 17,882 in the MALDI-TOF spectra were identified in lung tumor specimens as macrophage migration inhibitory factor and cyclophilin A, resp. Overexpression of both proteins was confirmed by Western blotting, and cyclophilin A was localized to the tumor cells by immunohistochem. These data demonstrate the feasibility of using a MALDI-TOF platform to generate protein expression profiles and identify potential mol. targets for ***cancer*** diagnostics and therapeutics.
ST protein expression profiling ***cancer*** MALDI TOF mass spectrometry; macrophage migration inhibitory factor overexpression nonsmall cell lung ***cancer*** ; cyclophilin A overexpression nonsmall cell lung ***cancer***
IT Cyclophilins
RL: ANT (Analyte); BSU (Biological study, unclassified); ANST (Analytical study); BIOL (Biological study)
(A; MALDI-TOF mass spectrometry protein expression profiling identifies macrophage migration inhibitory factor and cyclophilin A as overexpressed and potential mol. targets in non-small cell lung ***cancer***)
IT Human
(MALDI-TOF mass spectrometry protein expression profiling identifies macrophage migration inhibitory factor and cyclophilin A as overexpressed and potential mol. targets in non-small cell lung ***cancer***)
IT Macrophage migration inhibitory factor
RL: ANT (Analyte); BSU (Biological study, unclassified); ANST (Analytical study); BIOL (Biological study)
(MALDI-TOF mass spectrometry protein expression profiling identifies macrophage migration inhibitory factor and cyclophilin A as overexpressed and potential mol. targets in non-small cell lung ***cancer***)
IT Proteins
RL: ANT (Analyte); BSU (Biological study, unclassified); ANST (Analytical study); BIOL (Biological study)
(expression profiling; MALDI-TOF mass spectrometry protein expression profiling identifies macrophage migration inhibitory factor and cyclophilin A as overexpressed and potential mol. targets in non-small cell lung ***cancer***)
IT Time-of-flight mass spectrometry
(laser-induced photodesorption, matrix-assisted; MALDI-TOF mass spectrometry protein expression profiling identifies macrophage migration inhibitory factor and cyclophilin A as overexpressed and potential mol. targets in non-small cell lung ***cancer***)
IT Lung, neoplasm
(non-small-cell carcinoma; MALDI-TOF mass spectrometry protein expression profiling identifies macrophage migration inhibitory factor and cyclophilin A as overexpressed and potential mol. targets in non-small cell lung ***cancer***)
IT Laser ionization mass spectrometry
(photodesorption, matrix-assisted, time-of-flight; MALDI-TOF mass spectrometry protein expression profiling identifies macrophage migration inhibitory factor and cyclophilin A as overexpressed and potential mol. targets in non-small cell lung ***cancer***)
IT Laser desorption mass spectrometry
(photoionization, matrix-assisted, time-of-flight; MALDI-TOF mass spectrometry protein expression profiling identifies macrophage migration inhibitory factor and cyclophilin A as overexpressed and potential mol. targets in non-small cell lung ***cancer***)
IT Laser desorption mass spectrometry
(time-of-flight, matrix-assisted; MALDI-TOF mass spectrometry protein

and cyclophilin A as overexpressed and potential mol. targets in non-small cell lung ***cancer***)

RE.CNT 17 THERE ARE 17 CITED REFERENCES AVAILABLE FOR THIS RECORD
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L8 ANSWER 4 OF 11 CA COPYRIGHT 2004 ACS on STN
AN 138:363408 CA
ED Entered STN: 05 Jun 2003
TI ***Matrix*** - ***assisted*** ***laser*** ***desorption*** / ***ionization*** time-of-flight mass spectrometry-based detection of microsatellite instabilities in coding DNA sequences: A novel approach to identify DNA-mismatch repair-deficient ***cancer*** cells

AU Bonk, Thomas; Humeny, Andreas; Gebert, Johannes; Sutter, Christian; von Knebel Doeberitz, Magnus; Becker, Cord-Michael
CS Institut fur Biochemie, Emil-Fischer-Zentrum, Friedrich-Alexander Universitat Erlangen-Nurnberg, Erlangen, D-91054, Germany

SO Clinical Chemistry (Washington, DC, United States) (2003), 49(4), 552-561
CODEN: CLCHAU; ISSN: 0009-9147
PB American Association for Clinical Chemistry
DT Journal
LA English

CC 3-1 (Biochemical Genetics)
Section cross-reference(s): 9, 14

AB Inherited defects in the DNA mismatch repair system lead to increased loss or gain of repeat units in microsatellites, commonly referred to as microsatellite instability (MSI). MSIs in coding regions of crit. genes contribute to the pathogenesis of DNA-mismatch repair-deficient ***cancers*** , particularly those assocd. with the hereditary nonpolyposis colorectal ***cancer*** syndrome (HNPCC). MSI typing is therefore increasingly used to guide the mol. diagnosis of HNPCC. We used ***matrix*** - ***assisted*** ***laser*** ***desorption*** / ***ionization*** time-of-flight mass spectrometry (MALDI-TOF-MS) to identify MSIs in mononucleotide repeats within the coding sequences of genes relevant to the pathogenesis of MSI+ neoplastic lesions. After a primer extension reaction of PCR products encompassing the microsatellites, the mol. masses of the extension products were detd. by MALDI-TOF-MS. MSIs were detected by MALDI-TOF-MS in the GART, AC1, TGFBR2, MSH3, and MSH6 genes in neoplastic tissues and MSI+ colorectal ***cancer*** cell lines but not in MSI- control tissues. The anal. of peak-integral ratios in a single spectrum of the peaks representing insertions or deletions compared with the full-length microsatellites allowed relative quantification of MSIs. MALDI-TOF-MS-based genotyping results were confirmed by conventional DNA sequencing and electrophoresis. Because of its reliability, short run times, and low costs, this semiquant. procedure represents an effective alternative, in particular for ***diagnostic*** high-throughput typing of MSIs in neoplastic lesions.

ST MALDI TOF mass spectrometry genotyping microsatellite instability; coding DNA sequence DNA mismatch repair gene PCR ***cancer***
IT Gene, animal
RL: BSU (Biological study, unclassified); DGN (Diagnostic use); BIOL (Biological study); USES (Uses)
(AC1; MALDI-TOF mass spectrometry-based detection of microsatellite instabilities in coding DNA sequences to identify DNA-mismatch repair-deficient ***cancer*** cells)
IT Gene, animal
RL: BSU (Biological study, unclassified); DGN (Diagnostic use); BIOL (Biological study); USES (Uses)
(GART; MALDI-TOF mass spectrometry-based detection of microsatellite

repair-deficient ***cancer*** cells)
IT Human
PCR (polymerase chain reaction)
(MALDI-TOF mass spectrometry-based detection of microsatellite instabilities in coding DNA sequences to identify DNA-mismatch repair-deficient ***cancer*** cells)
IT Microsatellite DNA
RL: BSU (Biological study, unclassified); DGN (Diagnostic use); BIOL (Biological study); USES (Uses)
(MALDI-TOF mass spectrometry-based detection of microsatellite instabilities in coding DNA sequences to identify DNA-mismatch repair-deficient ***cancer*** cells)
IT DNA sequence analysis
Electrophoresis
(MALDI-TOF-MS-based genotyping results were confirmed by; MALDI-TOF mass spectrometry-based detection of microsatellite instabilities in coding DNA sequences to identify DNA-mismatch repair-deficient ***cancer*** cells)
IT Gene, animal
RL: BSU (Biological study, unclassified); DGN (Diagnostic use); BIOL (Biological study); USES (Uses)
(MSH3; MALDI-TOF mass spectrometry-based detection of microsatellite instabilities in coding DNA sequences to identify DNA-mismatch repair-deficient ***cancer*** cells)
IT Gene, animal
RL: BSU (Biological study, unclassified); DGN (Diagnostic use); BIOL (Biological study); USES (Uses)
(MSH6; MALDI-TOF mass spectrometry-based detection of microsatellite instabilities in coding DNA sequences to identify DNA-mismatch repair-deficient ***cancer*** cells)
IT Genotyping (method)
(MSI; MALDI-TOF mass spectrometry-based detection of microsatellite instabilities in coding DNA sequences to identify DNA-mismatch repair-deficient ***cancer*** cells)
IT Gene, animal
RL: BSU (Biological study, unclassified); DGN (Diagnostic use); BIOL (Biological study); USES (Uses)
(TGFBR2; MALDI-TOF mass spectrometry-based detection of microsatellite instabilities in coding DNA sequences to identify DNA-mismatch repair-deficient ***cancer*** cells)
IT Intestine, neoplasm
(colorectal, hereditary nonpolyposis; MALDI-TOF mass spectrometry-based detection of microsatellite instabilities in coding DNA sequences to identify DNA-mismatch repair-deficient ***cancer*** cells)
IT Time-of-flight mass spectrometry
(laser-induced photodesorption, matrix-assisted; MALDI-TOF mass spectrometry-based detection of microsatellite instabilities in coding DNA sequences to identify DNA-mismatch repair-deficient ***cancer*** cells)
IT DNA repair
(mismatch; MALDI-TOF mass spectrometry-based detection of microsatellite instabilities in coding DNA sequences to identify DNA-mismatch repair-deficient ***cancer*** cells)
IT Diagnosis
(mol.; MALDI-TOF mass spectrometry-based detection of microsatellite instabilities in coding DNA sequences to identify DNA-mismatch repair-deficient ***cancer*** cells)
IT Mass
(molar, of PCR product, by MALDI-TOF-MS; MALDI-TOF mass spectrometry-based detection of microsatellite instabilities in coding DNA sequences to identify DNA-mismatch repair-deficient ***cancer*** cells)
IT Laser ionization mass spectrometry
(photodesorption, matrix-assisted; MALDI-TOF mass spectrometry-based detection of microsatellite instabilities in coding DNA sequences to identify DNA-mismatch repair-deficient ***cancer*** cells)
IT Laser desorption mass spectrometry
(photoionization, matrix-assisted; MALDI-TOF mass spectrometry-based detection of microsatellite instabilities in coding DNA sequences to identify DNA-mismatch repair-deficient ***cancer*** cells)
IT Laser desorption mass spectrometry
(time-of-flight, matrix-assisted; MALDI-TOF mass spectrometry-based detection of microsatellite instabilities in coding DNA sequences to identify DNA-mismatch repair-deficient ***cancer*** cells)
RE.CNT 34 THERE ARE 34 CITED REFERENCES AVAILABLE FOR THIS RECORD
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L8 ANSWER 5 OF 11 CA COPYRIGHT 2004 ACS on STN
AN 137:58189 CA
ED Entered STN: 25 Jul 2002
TI Detection of tumor mutations in the presence of excess amounts of normal DNA
AU Sun, Xiyuan; Hung, K.; Wu, L.; Sidransky, D.; Guo, Baochuan
CS Dep. of Chemistry, Cleveland State University, Cleveland, OH, 44115, USA
SO Nature Biotechnology (2002), 20(2), 186-189
CODEN: NABIF9; ISSN: 1087-0156
PB Nature America Inc.
DT Journal
LA English
CC 3-1 (Biochemical Genetics)
Section cross-reference(s): 14
AB Mutations are important markers in the early detection of ***cancer*** . Clin. specimens such as bodily fluid samples often contain a small percentage of mutated cells in a large background of normal cells. Thus, assays to detect mutations leading to ***cancer*** need to be highly sensitive and specific. In addn., they should be possible to carry out in an automated and high-throughput manner to allow large-scale screening. Here we describe a screening method, termed PPEM (PNA-directed PCR, primer extension, MALDI-TOF), that addresses these needs more effectively than do existing methods. DNA samples are first amplified using peptide nucleic acid (PNA)-directed PCR clamping reactions in which mutated DNA is preferentially enriched. The PCR-amplified DNA fragments are then sequenced through primer extension to generate ***diagnostic*** products. Finally, mutations are identified using ***matrix*** - ***assisted*** ***laser*** - ***desorption*** / ***ionization*** time-of-flight (MALDI-TOF) mass spectrometry. This method can detect as few as 3 copies of mutant alleles in the presence of a 10,000-fold excess of normal alleles in a robust and specific manner. In addn., the method can be adapted for simultaneous detection of multiple mutations and is amenable to high-throughput automation.
ST peptide nucleic acid PCR sequencing MALDITOF diagnosis tumor mutation; gene Kras TP53 mutation lung ***cancer*** detection PPEM method
IT Primers (nucleic acid)
RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(DNA; method for detection of tumor mutations in the presence of excess amts. of normal DNA)
IT DNA sequence analysis
(MALDI-TOF; method for detection of tumor mutations in the presence of

IT Gene, animal
RL: ANT (Analyte); DGN (Diagnostic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(TP53; method for detection of tumor mutations in the presence of excess amts. of normal DNA)
IT Gene, animal
RL: ANT (Analyte); DGN (Diagnostic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(c-Ki-ras; method for detection of tumor mutations in the presence of excess amts. of normal DNA)
IT Mutation
(codon 12 of gene K-ras and codon 248 of gene TP53; method for detection of tumor mutations in the presence of excess amts. of normal DNA)
IT Time-of-flight mass spectrometry
(laser-induced photodesorption; method for detection of tumor mutations in the presence of excess amts. of normal DNA)
IT High throughput screening
Human
Lung, neoplasm
(method for detection of tumor mutations in the presence of excess amts. of normal DNA)
IT Peptide nucleic acids
RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(method for detection of tumor mutations in the presence of excess amts. of normal DNA)
IT p53 (protein)
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(method for detection of tumor mutations in the presence of excess amts. of normal DNA)
IT Diagnosis
(mol.; method for detection of tumor mutations in the presence of excess amts. of normal DNA)
IT PCR (polymerase chain reaction)
(multiplex, PNA-directed; method for detection of tumor mutations in the presence of excess amts. of normal DNA)
IT Ras proteins
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(p21v-Ki-ras; method for detection of tumor mutations in the presence of excess amts. of normal DNA)
IT Laser ionization mass spectrometry
(photodesorption, matrix-assisted; method for detection of tumor mutations in the presence of excess amts. of normal DNA)
IT Laser desorption mass spectrometry
(photoionization, matrix-assisted; method for detection of tumor mutations in the presence of excess amts. of normal DNA)
IT DNA
RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(primer; method for detection of tumor mutations in the presence of excess amts. of normal DNA)
IT Laser desorption mass spectrometry
(time-of-flight; method for detection of tumor mutations in the presence of excess amts. of normal DNA)
IT 439618-88-9D, 5'-biotinylated
RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(human gene K-ras specific PCR extension primer; method for detection of tumor mutations in the presence of excess amts. of normal DNA)
IT 439618-80-1 439618-81-2
RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(human gene K-ras specific PCR primer; method for detection of tumor mutations in the presence of excess amts. of normal DNA)
IT 439618-86-7
RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(human gene K-ras specific PNA PCR primer; method for detection of tumor mutations in the presence of excess amts. of normal DNA)
IT 439618-89-0
RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(human gene TP53 specific PCR extension primer; method for detection of tumor mutations in the presence of excess amts. of normal DNA)
IT 439618-82-3 439618-83-4

ANST (Analytical study); BIOL (Biological study); USES (Uses)
(human gene TP53 specific PCR primer; method for detection of tumor mutations in the presence of excess amts. of normal DNA)
IT 439618-87-8
RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(human gene TP53 specific PNA PCR primer; method for detection of tumor mutations in the presence of excess amts. of normal DNA)
IT 439618-84-5 439618-85-6
RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(human tumor mutation second-round PCR primer; method for detection of tumor mutations in the presence of excess amts. of normal DNA)
RE.CNT 20 THERE ARE 20 CITED REFERENCES AVAILABLE FOR THIS RECORD
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L8 ANSWER 6 OF 11 CA COPYRIGHT 2004 ACS on STN
AN 136:399500 CA
ED Entered STN: 20 Jun 2002
TI Proteome Analysis of Hepatocellular Carcinoma

AU Lim, Seung Oe; Park, Sung-Jun; Kim, Won; Park, Sung Gyoo; Kim, Hie-Joon; Kim, Yong-Il; Sohn, Tae-Sung; Noh, Jae-Hyung; Jung, Guhung
CS School of Biological Sciences, Seoul National University, Seoul, 151-747, S. Korea

SO Biochemical and Biophysical Research Communications (2002), 291(4), 1031-1037
CODEN: BBRCA9; ISSN: 0006-291X
PB Academic Press
DT Journal
LA English
CC 14-1 (Mammalian Pathological Biochemistry)

AB Development of hepatocellular carcinoma (HCC) is a complex process involving multiple changes in gene expression and usually occurs in the presence of liver cirrhosis. In this research, we obsd. proteome alterations of three tissue types isolated from livers of HCC patients: normal, cirrhotic, and tumorous tissue. Proteome alterations were obsd. using two-dimensional PAGE and ***matrix*** - ***assisted*** ***laser*** ***desorption*** / ***ionization*** time-of-flight mass spectrometry. Comparing the tissue types with each other, a significant change in expression level was found in 21 proteins. Of these proteins, sarcosine dehydrogenase, liver carboxylesterase, peptidyl-prolyl isomerase A, and lamin B1 are considered novel HCC marker candidates. In particular, lamin B1 may be considered as a marker for cirrhosis, because its expression level changes considerably in cirrhotic tissue compared with normal tissue. The proteins revealed in this expt. can be used in the future for studies pertaining to hepatocarcinogenesis, or as ***diagnostic*** markers and therapeutic targets for HCC. (c) 2002 Academic Press.

ST sarcosine dehydrogenase carboxylesterase lamin B1 hepatocellular carcinoma marker; peptidyl prolyl isomerase A liver cirrhosis hepatoma diagnosis
IT Annexins
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(A2; proteome anal. of hepatocellular carcinoma)
IT Proteins
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(FABP (fatty acid-binding protein); proteome anal. of hepatocellular

IT Proteins
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(GRP78 (glucose-regulated protein, 78 kDa); proteome anal. of hepatocellular carcinoma)
IT Phosphoproteins
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(HSC71 (heat-shock cognate, 71,000-mol.-wt.); proteome anal. of hepatocellular carcinoma)
IT Heat-shock proteins
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(HSP 60; proteome anal. of hepatocellular carcinoma)
IT Heat-shock proteins
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(HSP 70, HSP70RY; proteome anal. of hepatocellular carcinoma)
IT Heat-shock proteins
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(HSP 90.alpha.; proteome anal. of hepatocellular carcinoma)
IT Diagnosis
(***cancer*** ; proteome anal. of hepatocellular carcinoma)
IT Proteins
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(endoplasmins; proteome anal. of hepatocellular carcinoma)
IT Liver, neoplasm
(hepatoma; proteome anal. of hepatocellular carcinoma)
IT Proteins
RL: BSU (Biological study, unclassified); DGN (Diagnostic use); BIOL (Biological study); USES (Uses)
(lamins, B1; proteome anal. of hepatocellular carcinoma)
IT Proteins
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(nucleophosmin; proteome anal. of hepatocellular carcinoma)
IT Cirrhosis
Human
Tumor markers
(proteome anal. of hepatocellular carcinoma)
IT Vimentins
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(proteome anal. of hepatocellular carcinoma)
IT Tubulins
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(.beta.-, .beta.1; proteome anal. of hepatocellular carcinoma)
IT 207137-51-7, Peroxiredoxin
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(3; proteome anal. of hepatocellular carcinoma)
IT 95076-93-0, Peptidyl-prolyl isomerase
RL: BSU (Biological study, unclassified); DGN (Diagnostic use); BIOL (Biological study); USES (Uses)
(A; proteome anal. of hepatocellular carcinoma)
IT 9001-05-2, Catalase 9001-50-7, Glyceraldehyde 3-phosphate dehydrogenase 9028-86-8, Aldehyde dehydrogenase 9035-39-6, Cytochrome B5 37318-49-3, Protein disulfide isomerase
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(proteome anal. of hepatocellular carcinoma)
IT 9016-18-6, Carboxylesterase 37228-65-2, Sarcosine dehydrogenase
RL: BSU (Biological study, unclassified); DGN (Diagnostic use); BIOL (Biological study); USES (Uses)
(proteome anal. of hepatocellular carcinoma)
RE.CNT 31 THERE ARE 31 CITED REFERENCES AVAILABLE FOR THIS RECORD
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L8 ANSWER 7 OF 11 CA COPYRIGHT 2004 ACS on STN
AN 136:383614 CA
ED Entered STN: 13 Jun 2002
TI ***Cancer*** proteomics: New developments in clinical chemistry
AU Rai, A. J.; Chan, D. W.
CS Dept. of Pathology, Div. of Clinical Chemistry, The Johns Hopkins University School of Medicine, Baltimore, MD, 21287, USA
SO Laboratoriumsmedizin (2001), 25(9-10), 399-403
CODEN: LABOD3; ISSN: 0342-3026
PB Blackwell Wissenschafts-Verlag GmbH
DT Journal; General Review
LA English
CC 14-0 (Mammalian Pathological Biochemistry)
AB A review. The entire protein complement of a cell is termed the proteome. "Proteomics" is defined as the systematic expression of diverse properties of proteins in a cell. Proteomic methodologies can detect protein modifications, which occur after protein synthesis. The anal. of the proteome thus provides useful information, which can be used for the identification and screening of ***diagnostic*** markers, and is relevant for the understanding of tumor-progression. In past years, the most widely used tool of proteome-anal. was 2D-gel electrophoresis. Today, new methods are available, which are based on biochip technol. High affinity surface-binding arrays can analyze epitopes of complex protein matrixes and specify functional aspects of tumor-progression. After initial isolation, the sepd. proteins are identified by mass spectrometry based techniques such as MALDI (***matrix*** ***assisted*** ***laser*** ***desorption*** ***ionization***) or SELDI (surface enhanced laser desorption ionization) - TOF (time of flight). This review focuses on new developments in proteomics, including SELDI, and describes applications of these methods for the search of new "protein signatures" in ***cancer*** research. It is expected that the advancements of proteomics-techniques will help to classify human ***cancer*** by mol. rather than morphol. characteristics.
ST review human ***cancer*** marker proteome
IT DNA microarray technology
Human
Mass spectrometry
Neoplasm
Tumor markers
(***cancer*** proteomics, new developments in clin. chem.)
IT Proteome
RL: ADV (Adverse effect, including toxicity); DGN (Diagnostic use); PRP (Properties); BIOL (Biological study); USES (Uses)
(***cancer*** proteomics, new developments in clin. chem.)
RE.CNT 9 THERE ARE 9 CITED REFERENCES AVAILABLE FOR THIS RECORD
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L8 ANSWER 8 OF 11 CA COPYRIGHT 2004 ACS on STN
AN 136:259444 CA
ED Entered STN: 18 Apr 2002
TI Analysis of the saliva from patients with oral ***cancer*** by ***matrix*** - ***assisted*** ***laser*** ***desorption*** /

AU Chen, Yu-Chie; Li, Tzu-Ying; Tsai, Ming-Fei
CS Department of Applied Chemistry, National Chiao Tung University, Hsinchu, 300, Taiwan
SO Rapid Communications in Mass Spectrometry (2002), 16(5), 364-369
CODEN: RCMSEF; ISSN: 0951-4198
PB John Wiley & Sons Ltd.
DT Journal
LA English
CC 9-5 (Biochemical Methods)
Section cross-reference(s): 14
AB Using ***matrix*** - ***assisted*** ***laser*** ***desorption*** / ***ionization*** mass spectrometry (MALDI-MS), this study analyzed the saliva obtained from patients with oral ***cancer*** and compared these mass spectra with those obtained from healthy controls. Saliva without pre-treatment was mixed directly with a sinapinic acid matrix. Alpha-amylase (57 kDa) dominated the high mass range in the MALDI mass spectra of the saliva from healthy subjects, but the peak was suppressed for patients with oral ***cancer*** and was replaced by a peak at m/z 66 k in the spectra of patients' samples (15 out of 20). Sodium dodecyl sulfate PAGE (SDS-PAGE) with in-gel tryptic digestion combined with ***matrix*** - ***assisted*** ***laser*** ***desorption*** / ***ionization*** time-of-flight (MALDI-TOF) was employed to characterize this 66-kDa protein, which was thus shown to be albumin. However, based on SDS-PAGE results, concns. of both alpha-amylase and albumin in patients' saliva were significantly higher than those in healthy subjects. This discrepancy was shown to be due to MALDI suppression effects due to the albumin. MALDI-MS thus has potential as a possible rapid ***diagnostic*** screening tool for oral ***cancer*** .
ST saliva mouth ***cancer*** MALDI TOF mass spectrometry
IT Diagnosis
(agents; saliva anal. from patients with oral ***cancer*** by ***matrix*** - ***assisted*** ***laser*** ***desorption*** / ***ionization*** time-of-flight mass spectrometry)
IT Laser ionization mass spectrometry
(photodesorption, matrix-assisted; saliva anal. from patients with oral ***cancer*** by ***matrix*** - ***assisted*** ***laser*** ***desorption*** / ***ionization*** time-of-flight mass spectrometry)
IT Laser desorption mass spectrometry
(photoionization, matrix-assisted; saliva anal. from patients with oral ***cancer*** by ***matrix*** - ***assisted*** ***laser*** ***desorption*** / ***ionization*** time-of-flight mass spectrometry)
IT Blood analysis
Gel electrophoresis
Human
Mouth, neoplasm
Saliva
Sex
Time-of-flight mass spectrometry
(saliva anal. from patients with oral ***cancer*** by ***matrix*** - ***assisted*** ***laser*** ***desorption*** / ***ionization*** time-of-flight mass spectrometry)
IT Albumins, analysis
Proteins
RL: ANT (Analyte); DGN (Diagnostic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(saliva anal. from patients with oral ***cancer*** by ***matrix*** - ***assisted*** ***laser*** ***desorption*** / ***ionization*** time-of-flight mass spectrometry)
IT Blood-group substances
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(saliva anal. from patients with oral ***cancer*** by ***matrix*** - ***assisted*** ***laser*** ***desorption*** / ***ionization*** time-of-flight mass spectrometry)
IT 9000-90-2, .alpha.-Amylase
RL: ANT (Analyte); DGN (Diagnostic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(saliva anal. from patients with oral ***cancer*** by ***matrix*** - ***assisted*** ***laser*** ***desorption*** / ***ionization*** time-of-flight mass spectrometry)
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L8 ANSWER 9 OF 11 CA COPYRIGHT 2004 ACS on STN
AN 136:230303 CA
ED Entered STN: 04 Apr 2002
TI Serum protein profiles of patients with pancreatic ***cancer*** and chronic pancreatitis: searching for a ***diagnostic*** protein pattern
AU Valerio, A.; Basso, D.; Mazza, S.; Baldo, G.; Tiengo, A.; Pedrazzoli, S.; Seraglia, R.; Plebani, M.
CS Department of Clinical and Experimental Medicine, University of Padova, Italy
SO Rapid Communications in Mass Spectrometry (2001), 15(24), 2420-2425
CODEN: RCMSEF; ISSN: 0951-4198
PB John Wiley & Sons Ltd.
DT Journal
LA English
CC 14-1 (Mammalian Pathological Biochemistry)
AB In this study, 13 sera from patients with pancreatic ***cancer*** , 9 from chronic pancreatitis and 10 from healthy subjects were analyzed by ***matrix*** - ***assisted*** ***laser*** ***desorption*** / ***ionization*** (MALDI) mass spectrometry. The MALDI mass spectra revealed the presence of several low mol. wt. peptides, among which some were detected only in the sera from both pathol. conditions. On the other hand many peptides were obsd. only in control sera, and were absent in the sera from the two diseases. Therefore, MALDI anal. of the low mol. wt. fraction (<10000 Da) of sera from patients with pancreatic diseases enabled us to identify the presence of some disease-related signals and also some signals characteristic of normal subjects.
ST ***diagnostic*** blood protein profile pancreas ***cancer*** pancreatitis
IT Proteins
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(blood, profiles; serum protein profiles of human patients with pancreatic ***cancer*** and chronic pancreatitis and searching for a ***diagnostic*** protein pattern)
IT Pancreas, disease
(chronic pancreatitis; serum protein profiles of human patients with pancreatic ***cancer*** and chronic pancreatitis and searching for a ***diagnostic*** protein pattern)
IT Molecular weight
(low, fraction; serum protein profiles of human patients with pancreatic ***cancer*** and chronic pancreatitis and searching for a ***diagnostic*** protein pattern)
IT Laser ionization mass spectrometry
(photodesorption, matrix-assisted; serum protein profiles of human patients with pancreatic ***cancer*** and chronic pancreatitis and searching for a ***diagnostic*** protein pattern)
IT Laser desorption mass spectrometry
(photoionization, matrix-assisted; serum protein profiles of human patients with pancreatic ***cancer*** and chronic pancreatitis and searching for a ***diagnostic*** protein pattern)

(serum protein profiles of human patients with pancreatic ***cancer*** and chronic pancreatitis and searching for a ***diagnostic*** protein pattern)
IT Signal peptides
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(serum protein profiles of human patients with pancreatic ***cancer*** and chronic pancreatitis and searching for a ***diagnostic*** protein pattern)
RE.CNT 14 THERE ARE 14 CITED REFERENCES AVAILABLE FOR THIS RECORD
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L8 ANSWER 10 OF 11 CA COPYRIGHT 2004 ACS on STN
AN 131:183059 CA
ED Entered STN: 25 Sep 1999
TI Proteomics in human disease. ***Cancer*** , heart, and infectious diseases
AU Jungblut, Peter R.; Zimny-Arndt, Ursula; Zeindl-Eberhart, Evelyn; Stulik, Jiri; Koupilova, Kamila; Pleissner, Klaus-Peter; Otto, Albrecht; Muller, Eva-Christina; Sokolowska-Kohler, Wanda; Grabher, Gertrud; Stoffler, Georg
CS Protein Analyse Einheit, Max-Planck-Institut Infektionsbiologie, Berlin, D-10117, Germany
SO Electrophoresis (1999), 20(10), 2100-2110
CODEN: ELCTDN; ISSN: 0173-0835
PB Wiley-VCH Verlag GmbH
DT Journal; General Review
LA English
CC 14-0 (Mammalian Pathological Biochemistry)
Section cross-reference(s): 9
AB A review with 66 refs. is given on proteomics, a rapidly growing research area that encompasses both genetic and environmental factors. In recent years, genomics has increased the understanding of many diseases. The protein compn. represents the functional status of a biol. compartment. The 5 approaches presented here resulted in the detection of disease-assocd. proteins. Calgranulin B was upregulated in colorectal ***cancer*** , and hepatoma-derived aldose reductase-like protein was reexpressed in a rat model during hepatocarcinogenesis. In these 2 investigations, attention was focused on 1 protein, obviously differing in amt., directly after 2-dimensional electrophoresis (2-DE). Addnl. methods, such as enzyme activity measurements and immunohistochem., confirmed the disease assocn. of the 2 candidates resulting from 2-DE subtractive anal. The following 3 investigations take advantage of the holistic potential of the 2-DE approach. The comparison of 2-DE patterns from dilated cardiomyopathy patients with those of controls revealed 25 intensity differences, from which 12 were identified by amino acid anal., Edman degrdn., or ***matrix*** - ***assisted*** ***laser*** ***desorption*** / ***ionization*** -mass spectrometry (MALDI-MS). A human myocardial 2-DE database was constructed, contg. 3300 protein spots and 150 identified protein species. The no. of identified proteins was limited by the capacity of the authors group, rather than by the principle of feasibility. Another field where proteomics proves to be a valuable tool in identifying proteins of importance for diagnosis is proteome anal. of pathogenic microorganisms such as Borrelia burgdorferi (Lyme disease) and Toxoplasma gondii (toxoplasmosis). Blood sera from patients with early or late symptoms of Lyme borreliosis contained antibodies of various classes against about 80 antigens each, contg. the already described antigens OspA, B and C, flagellin, p83/100, and p39. Similarly, antibody reactivity to 7 different marker antigens of T. gondii allowed differentiation between acute and latent toxoplasmosis, an important ***diagnostic*** tool in both pregnancy and immunosuppressed patients.
ST review disease assocd protein ***diagnostic*** electrophoresis
IT Heart, disease
(cardiomyopathy; detection and characterization of disease-assocd.

IT Intestine, neoplasm
(colorectal; detection and characterization of disease-assocd. proteins)
IT Borrelia
(detection and characterization of disease-assocd. proteins)
IT Proteins, specific or class
RL: ANT (Analyte); BOC (Biological occurrence); BSU (Biological study, unclassified); ANST (Analytical study); BIOL (Biological study); OCCU (Occurrence)
(detection and characterization of disease-assocd. proteins)
IT Liver, neoplasm
(hepatoma; detection and characterization of disease-assocd. proteins)
IT Toxoplasma gondii
(toxoplasmosis from; detection and characterization of disease-assocd. proteins)
IT Proteins, specific or class
RL: ANT (Analyte); BOC (Biological occurrence); BSU (Biological study, unclassified); ANST (Analytical study); BIOL (Biological study); OCCU (Occurrence)
(tumor-assocd.; detection and characterization of disease-assocd. proteins)
IT Electrophoresis
(two-dimensional; detection and characterization of disease-assocd. proteins)
RE.CNT 66 THERE ARE 66 CITED REFERENCES AVAILABLE FOR THIS RECORD
RE

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L8 ANSWER 11 OF 11 CA COPYRIGHT 2004 ACS on STN
AN 131:15954 CA
ED Entered STN: 03 Jul 1999
TI Identification of proteins in a human pleural exudate using 2-dimensional preparative liquid-phase electrophoresis and ***matrix*** - ***assisted*** ***laser*** ***desorption*** / ***ionization*** mass spectrometry
AU Nilsson, Carol Lynn; Puchades, Maja; Westman, Ann; Biennow, Kaj; Davidsson, Pia
CS Department Clinical Neuroscience, Unit Neurochemistry, Sahlgrenska Hospital, Moelndal, S-43180, Swed.
SO Electrophoresis (1999), 20(4-5), 860-865
CODEN: ELCTDN; ISSN: 0173-0835
PB Wiley-VCH Verlag GmbH
DT Journal
LA English
CC 9-7 (Biochemical Methods)
Section cross-reference(s): 14
AB Pleural effusion may occur in patients suffering from phys. trauma or systemic disorders such as infection, inflammation, or ***cancer***. To investigate proteins in a pleural exudate from a patient with severe pneumonia, the authors used a strategy that combined preparative 2-D liq.-phase electrophoresis (2-D LPE), ***matrix*** - ***assisted*** ***laser*** ***desorption*** / ***ionization*** time-of-flight mass spectrometry (MALDI-TOF-MS) and Western blotting. Preparative 2-D LPE is based on the same principles as anal. 2-D gel electrophoresis, except that the proteins remain in liq. phase during the entire procedure. In the 1st dimension, liq.-phase isoelec. focusing allows for the enrichment of proteins in liq. fractions. In the Rotofor cell, large vols. (.ltoreq.55 mL) and protein amts. (.ltoreq.1-2 g) can be loaded. Several low abundance proteins, cystatin C, haptoglobin, transthyretin, .beta.2-microglobulin, and transferrin, were detected after liq.-phase isoelec. focusing, through Western blotting, in a pleural exudate (by definition, >25 g/L total protein). Direct MALDI-TOF-MS anal. of proteins in a Rotofor fraction is demonstrated as well. MALDI-TOF-MS anal. of a tryptic digest of a continuous elution Na dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE) fraction confirmed the presence of cystatin C. By applying 2-D LPE, MALDI-TOF-MS, and Western blotting the authors confirmed the identity of proteins of potential ***diagnostic*** value. These findings serve to illustrate the usefulness of this combination of methods in the anal. of pathol. fluids.
ST protein pleural exudate liq electrophoresis MALDI TOF mass spectrometry
IT Laser ionization mass spectrometry
(photodesorption, matrix-assisted; proteins in pleural exudate investigated by 2-D preparative liq.-phase electrophoresis and ***matrix*** - ***assisted*** ***laser*** ***desorption*** / ***ionization*** mass spectrometry)
IT Laser desorption mass spectrometry
(photoionization, matrix-assisted; proteins in pleural exudate investigated by 2-D preparative liq.-phase electrophoresis and ***matrix*** - ***assisted*** ***laser*** ***desorption*** / ***ionization*** mass spectrometry)
IT Gel electrophoresis
(preparative; proteins in pleural exudate investigated by 2-D preparative liq.-phase electrophoresis and ***matrix*** - ***assisted*** ***laser*** ***desorption*** / ***ionization*** mass spectrometry)
IT Pleural fluid

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      electrophoresis and   ***matrix***  -  ***assisted***     ***laser***
        ***desorption***  /  ***ionization***   mass spectrometry)
IT   Haptoglobin
     Hemoglobins
     Proteins, specific or class
     Transferrins
     Transthyretin
     RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL
     (Biological study); PROC (Process)
        (proteins in pleural exudate investigated by 2-D preparative liq.-phase
        electrophoresis and   ***matrix***  -  ***assisted***     ***laser***
        ***desorption***  /  ***ionization***   mass spectrometry)
IT   Gel electrophoresis
        (two-dimensional; proteins in pleural exudate investigated by 2-D
        preparative liq.-phase electrophoresis and   ***matrix***  -
        ***assisted***     ***laser***     ***desorption***  /
        ***ionization***   mass spectrometry)
IT   Microglobulins
     RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL
     (Biological study); PROC (Process)
        (.beta.2-; proteins in pleural exudate investigated by 2-D preparative
        liq.-phase electrophoresis and   ***matrix***  -  ***assisted***
        ***laser***     ***desorption***  /  ***ionization***   mass
        spectrometry)
IT   91448-99-6, Cystatin C
     RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL
     (Biological study); PROC (Process)
        (proteins in pleural exudate investigated by 2-D preparative liq.-phase
        electrophoresis and   ***matrix***  -  ***assisted***     ***laser***
        ***desorption***  /  ***ionization***   mass spectrometry)
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     (FILE 'HOME' ENTERED AT 20:07:32 ON 11 JAN 2004)

     FILE 'CA' ENTERED AT 20:07:40 ON 11 JAN 2004
L1             1 S SURFACE(W)ENHANCED(W)NEAT(W)DESORPTION
L2           118 S SURFACE(W)ENHANCED(W)LASER(W)DESORPTION(W)IONIZATION
L3            20 S L2 AND DIAGNOSTIC
L4          4940 S MATRIX(W)ASSISTED(W)LASER(W)DESORPTION(W)IONIZATION
L5            66 S L4 AND DIAGNOSTIC
L6             0 S L5 AND CATIONIC(W)ADSORBENT?
L7             0 S L5 AND CATIONIC
L8            11 S L5 AND CANCER?

=> s l3 and cancer?
        201839 CANCER?
L9          11 L3 AND CANCER?

=> d all 1-11

L9   ANSWER 1 OF 11  CA  COPYRIGHT 2004 ACS on STN
AN   139:321232  CA
ED   Entered STN:  13 Nov 2003
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AU Lehrer, S.; Roboz, J.; Ding, H.; Zhao, S.; Diamond, E. J.; Holland, J. F.; Stone, N. N.; Droller, M. J.; Stock, R. G.
CS Department of Radiation Oncology, Mount Sinai School of Medicine, New York, NY, USA
SO BJU International (2003), 92(3), 223-225
CODEN: BJINFO; ISSN: 1464-4096
PB Blackwell Publishing Ltd.
DT Journal
LA English
CC 14-1 (Mammalian Pathological Biochemistry)
AB OBJECTIVE To describe the preliminary identification of serum proteins that may be ***diagnostic*** markers in prostate ***cancer*** . PATIENTS AND METHODS The study included 11 men referred for treatment of localized prostate ***cancer*** , 12 with benign prostatic hyperplasia (BPH) and 12 disease-free controls. For serum protein anal., the protein-chip array ***surface*** - ***enhanced*** ***laser*** ***desorption*** / ***ionization*** (SELDI) technique was used (Ciphergen Biosystems, Fremont, CA). SELDI combines protein-chip technol. with time-of-flight mass spectrometry, and offers the advantages of speed, simplicity and sensitivity. RESULTS Three protein peaks were identified in the serum of men with prostate ***cancer*** and BPH, but not in controls, with relative mol. masses of 15.2, 15.9 and 17.5 kDa. These three proteins were significantly assocd. with BPH and prostate ***cancer*** when compared with controls (P = 0.001, 0.004, and 0.011, resp., Kruskal-Wallis test). Interestingly, the 17.5 kDa protein was more abundant in five men with stage T1 prostate ***cancer*** than in eight with stage T2 (P= 0.016, two tailed Mann-Whitney U-test cor. for ties). CONCLUSIONS These proteins, particularly the 15.9 kDa one, may be used for the diagnosis or monitoring of prostate ***cancer*** and differentiation from BPH, and have the potential for antibody-based chip SELDI-TOF technol. Identified proteins may be targets for immunotherapy.
ST prostate ***cancer*** serum protein tumor marker
IT Proteins
RL: BSU (Biological study, unclassified); DGN (Diagnostic use); BIOL (Biological study); USES (Uses)
(15.2 kDa; putative protein markers in the sera of men with prostatic neoplasms)
IT Proteins
RL: BSU (Biological study, unclassified); DGN (Diagnostic use); BIOL (Biological study); USES (Uses)
(15.9 kDa; putative protein markers in the sera of men with prostatic neoplasms)
IT Proteins
RL: BSU (Biological study, unclassified); DGN (Diagnostic use); BIOL (Biological study); USES (Uses)
(17.5 kDa; putative protein markers in the sera of men with prostatic neoplasms)
IT Proteins
RL: BSU (Biological study, unclassified); DGN (Diagnostic use); BIOL (Biological study); USES (Uses)
(blood; putative protein markers in the sera of men with prostatic neoplasms)
IT Human
Prostate gland, neoplasm
Tumor markers
(putative protein markers in the sera of men with prostatic neoplasms)
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L9 ANSWER 2 OF 11 CA COPYRIGHT 2004 ACS on STN
AN 138:299912 CA
ED Entered STN: 08 May 2003
TI Clinical potential of proteomics in the diagnosis of ovarian ***cancer***
AU Ardekani, Ali M.; Liotta, Lance A.; Petricoin, Emanuel, III
CS Proteomics Unit, Bethesda, MD, 20892, USA
SO Expert Review of Molecular Diagnostics (2002), 2(4), 312-320
CODEN: ERMDCW; ISSN: 1473-7159
PB Future Drugs Ltd.

LA English
CC 9-0 (Biochemical Methods)
AB A review. The need for specific and sensitive markers of ovarian ***cancer*** is crit. Finding a sensitive and specific test for its detection has an important public health impact. Currently, there are no effective screening options available for patients with ovarian ***cancer*** . CA-125, the most widely used biomarker for ovarian ***cancer*** , does not have a high pos. predictive value and it is only effective when used in combination with other ***diagnostic*** tests. However, pathol. changes taking place within the ovary may be reflected in biomarker patterns in the serum. Combination of mass spectra generated by new proteomic technologies, such as ***surface*** - ***enhanced*** ***laser*** ***desorption*** ***ionization*** time-of-flight (SELDI-TOF) and artificial-intelligence-based informatic algorithms, have been used to discover a small set of key protein values and discriminate normal from ovarian ***cancer*** patients. Serum proteomic pattern anal. might be applied ultimately in medical screening clinics, as a supplement to the ***diagnostic*** work-up and evaluation.
ST review proteomics diagnosis ovarian ***cancer***
IT Diagnosis
Human
Mass spectrometry
Ovary, neoplasm
(clin. potential of proteomic technologies in diagnosis of ovarian ***cancer***)
IT CA 125 (carbohydrate antigen)
RL: DGN (Diagnostic use); BIOL (Biological study); USES (Uses)
(clin. potential of proteomic technologies in diagnosis of ovarian ***cancer***)
IT Algorithm
(genetic; clin. potential of proteomic technologies in diagnosis of ovarian ***cancer***)
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L9 ANSWER 3 OF 11 CA COPYRIGHT 2004 ACS on STN
AN 138:35534 CA
ED Entered STN: 16 Jan 2003
TI Analysis of microdissected prostate tissue with ProteinChip arrays - a way to new insights into carcinogenesis and to ***diagnostic*** tools
AU Wellmann, Axel; Wollscheid, Volker; Lu, Hong; Ma, Zhan Lu; Albers, Peter; Schutze, Karin; Rohde, Volker; Behrens, Peter; Dreschers, Stefan; Ko, Yon; Wernert, Nicolas
CS Institute of Pathology, University of Bonn, Bonn, D-53127, Germany
SO International Journal of Molecular Medicine (2002), 9(4), 341-347
CODEN: IJMMFG; ISSN: 1107-3756
PB International Journal of Molecular Medicine
DT Journal
LA English
CC 9-5 (Biochemical Methods)
Section cross-reference(s): 14
AB Prostate carcinomas are one of the most common malignancies in western societies. The pathogenesis of this tumor is still poorly understood. These tumors present with two characteristic features: epithelial-mesenchymal interactions, which play a pivotal role for tumor development and most of clin. manifest ***cancers*** arise in prostate proper compared to a minority of tumors which develop in the transitional zone. Deciphering the epithelial-mesenchymal cross talk and identification of mol. pecularities of the sub-populations of cells in different zones can therefore help understanding carcinogenesis and development of new, non-invasive tools for the diagnosis and prognosis of prostate carcinomas which has remained a challenge until today. A ProteinChip array technol. (SELDI = ***surface*** ***enhanced*** ***laser*** ***desorption*** ***ionization***) has been developed recently by Ciphergen Biosystems enabling anal. and profiling of complex protein mixts. from a few cells. This study describes the anal. of approx. 500-1000 freshly obtained prostate cells by SELDI-TOF-MS (***surface*** ***enhanced*** ***laser*** ***desorption*** ***ionization*** time-of-flight mass spectrometry). Pure cell populations of stroma, epithelium and tumor cells were selected by laser assisted microdissection. Multiple specific protein patterns were reproducibly detected in the range from 1.5 to 30 kDa in 28 sub-populations of 4 tumorous prostates and 1 control. A specific 4.3 kDa peak was increased in the prostate tumor stroma compared to normal prostate proper and transitional zone stroma and increased in prostate tumor glands compared to normal prostate proper and transitional zone glands. Coupling laser assisted microdissection with SELDI provides tremendous opportunities to identify cell and tumor specific proteins to understand mol. events underlying prostate carcinoma development. It underlines the vast potential of this technol. to better understand pathogenesis and identify potential candidates for new specific biomarkers in general which could help to screen for and distinguish disease entities, i.e. between clin. significant and insignificant carcinomas of the prostate.
ST prostate ***cancer*** tissue protein chip array SELDI TOF
IT Time-of-flight mass spectrometry
(SELDI-TOF; anal. of microdissected prostate tissue with ProteinChip arrays as a way to new insights into carcinogenesis and to ***diagnostic*** tools)
IT Diagnosis
(agents; anal. of microdissected prostate tissue with ProteinChip arrays as a way to new insights into carcinogenesis and to ***diagnostic*** tools)
IT Animal tissue
Prostate gland, neoplasm
Protein microarray technology
Transformation, neoplastic
(anal. of microdissected prostate tissue with ProteinChip arrays as a way to new insights into carcinogenesis and to ***diagnostic*** tools)
IT Laser cutting
(laser assisted microdissection; anal. of microdissected prostate tissue with ProteinChip arrays as a way to new insights into carcinogenesis and to ***diagnostic*** tools)
IT Laser ionization mass spectrometry
(photodesorption, surface-enhanced, SELDI-TOF; anal. of microdissected prostate tissue with ProteinChip arrays as a way to new insights into

IT Laser desorption mass spectrometry
(photoionization, surface-enhanced, SELDI-TOF; anal. of microdissected prostate tissue with ProteinChip arrays as a way to new insights into carcinogenesis and to ***diagnostic*** tools)

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L9 ANSWER 4 OF 11 CA COPYRIGHT 2004 ACS on STN

AN 137:383041 CA
ED Entered STN: 19 Dec 2002

TI Normal, benign, preneoplastic, and malignant prostate cells have distinct protein expression profiles resolved by ***surface*** ***enhanced*** ***laser*** ***desorption*** / ***ionization*** mass spectrometry

AU Cazares, Lisa H.; Adam, Bao-Ling; Ward, Michael D.; Nasim, Suhail; Schellhammer, Paul F.; Semmes, O. John; Wright, George L., Jr.

CS Departments of Microbiology and Molecular Cell Biology, Eastern Virginia Medical School and Sentara Cancer Institute, Norfolk, VA, 23501, USA

SO Clinical Cancer Research (2002), 8(8), 2541-2552
CODEN: CCREF4; ISSN: 1078-0432

PB American Association for Cancer Research

DT Journal

LA English

CC 14-1 (Mammalian Pathological Biochemistry)

AB Purpose: The objective of this study was to discover protein biomarkers that differentiate malignant from non-malignant cell populations, esp. early protein alterations that signal the initiation of a developing ***cancer*** . The authors hypothesized that ***Surface*** ***Enhanced*** ***Laser*** ***Desorption*** / ***Ionization*** -time of flight-mass spectrometry-assisted protein profiling could detect these protein alterations. Exptl. Design: Epithelial cell populations [benign prostatic hyperplasia (BPH), prostate intraepithelial neoplasia (PIN), and prostate ***cancer*** (PCA)] were procured from nine prostatectomy specimens using laser capture microdissection. ***Surface*** ***Enhanced*** ***Laser*** ***Desorption*** / ***Ionization*** -time of flight-mass spectrometry anal. was performed on cell lysates, and the relative intensity levels of each protein or peptide in the mass spectra was calcd. and compared for each cell type. Results: Several small mol. mass peptides or proteins (3000-5000 Da) were found in greater abundance in PIN and PCA cell lysates. Another peak, with an av. mass of 5666 Da, was obsd. to be up-regulated in 86% of the BPH cell lysates. Higher levels of this same peak were found in only 22% of the PIN lysates and none of the PCA lysates. Expression differences were also found for intracellular levels of prostate-specific antigen, which were reduced in PIN and PCA cells when compared with matched normals. Although no single protein alteration was obsd. in all PIN/PCA samples, combining two or more of the markers was effective in distinguishing the benign cell types (normal/BPH) from diseased cell types (PIN/PCA). Logistic regression anal. using seven differentially expressed proteins resulted in a predictive equation that correctly distinguished the diseased lysates with a sensitivity and specificity of 93.3 and 93.8%, resp. Conclusions: We have shown that the protein profiles from prostate cells with different disease states have discriminating differences. These differentially regulated proteins are potential markers for early detection and/or risk factors for development of prostate ***cancer*** . Studies are under way to identify these protein/peptides, with the goal of developing a ***diagnostic*** test for the early detection of prostate ***cancer***

ST protein expression profile prostate hyperplasia ***cancer***

(benign hyperplasia; normal, benign, preneoplastic, and malignant prostate cells have distinct protein expression profiles resolved by ***surface*** ***enhanced*** ***laser*** ***desorption*** / ***ionization*** mass spectrometry)

IT Diagnosis
(***cancer*** ; normal, benign, preneoplastic, and malignant prostate cells have distinct protein expression profiles resolved by ***surface*** ***enhanced*** ***laser*** ***desorption*** / ***ionization*** mass spectrometry)

IT Human
Prostate gland, neoplasm
Tumor markers
(normal, benign, preneoplastic, and malignant prostate cells have distinct protein expression profiles resolved by ***surface*** ***enhanced*** ***laser*** ***desorption*** / ***ionization*** mass spectrometry)

IT Prostate-specific antigen
Proteins
Proteome
RL: BSU (Biological study, unclassified); DGN (Diagnostic use); BIOL (Biological study); USES (Uses)
(normal, benign, preneoplastic, and malignant prostate cells have distinct protein expression profiles resolved by ***surface*** ***enhanced*** ***laser*** ***desorption*** / ***ionization*** mass spectrometry)

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L9 ANSWER 5 OF 11 CA COPYRIGHT 2004 ACS on STN
AN 137:259585 CA
ED Entered STN: 24 Oct 2002
TI Proteomics and bioinformatics approaches for identification of serum biomarkers to detect breast ***cancer***

AU Li, Jinong; Zhang, Zhen; Rosenzweig, Jason; Wang, Young Y.; Chan, Daniel W.
CS Department of Pathology, Johns Hopkins Medical Institutions, Baltimore,

SO Clinical Chemistry (Washington, DC, United States) (2002), 48(8), 1296-1304
CODEN: CLCHAU; ISSN: 0009-9147
PB American Association for Clinical Chemistry
DT Journal
LA English
CC 9-16 (Biochemical Methods)
Section cross-reference(s): 14
AB Background: ***Surface*** - ***enhanced*** ***laser*** ***desorption*** / ***ionization*** (SELDI) is an affinity-based mass spectrometric method in which proteins of interest are selectively adsorbed to a chem. modified surface on a biochip, whereas impurities are removed by washing with buffer. This technol. allows sensitive and high-throughput protein profiling of complex biol. specimens. Methods: We screened for potential tumor biomarkers in 169 serum samples, including samples from a ***cancer*** group of 103 breast ***cancer*** patients at different clin. stages [stage 0 (n = 4), stage I (n = 38), stage II (n = 37), and stage III (n = 24)], from a control group of 41 healthy women, and from 25 patients with benign breast diseases. Dild. serum samples were applied to immobilized metal affinity capture Ciphergen Protein Chip Arrays previously activated with Ni2+. Proteins bound to the chelated metal were analyzed on a ProteinChip Reader Model PBS II. Complex protein profiles of different ***diagnostic*** groups were compared and analyzed using the Pro Peak software package. Results: A panel of three biomarkers was selected based on their collective contribution to the optimal sepn. between stage 0-I breast ***cancer*** patients and non- ***cancer*** controls. The same sepn. was obsd. using independent test data from stage II-III breast ***cancer*** patients. Bootstrap cross-validation demonstrated that a sensitivity of 93% for all ***cancer*** patients and a specificity of 91% for all controls were achieved by a composite index derived by multivariate logistic regression using the three selected biomarkers. Conclusions: Proteomics approaches such as SELDI mass spectrometry, in conjunction with bioinformatics tools, could greatly facilitate the discovery of new and better biomarkers. The high sensitivity and specificity achieved by the combined use of the selected biomarkers show great potential for the early detection of breast ***cancer*** .
ST proteome bioinformatic serum biomarker detect breast ***cancer***
IT Laser ionization mass spectrometry
(photodesorption, surface-enhanced; proteomics and bioinformatics approaches for identification of serum biomarkers to detect breast ***cancer***)
IT Laser desorption mass spectrometry
(photoionization, surface-enhanced; proteomics and bioinformatics approaches for identification of serum biomarkers to detect breast ***cancer***)
IT Bioinformatics
Biomarkers (biological responses)
Blood serum
High throughput screening
Human
Mammary gland, neoplasm
Simulation and Modeling, biological
Statistical analysis
(proteomics and bioinformatics approaches for identification of serum biomarkers to detect breast ***cancer***)
IT Proteins
RL: ANT (Analyte); BSU (Biological study, unclassified); DGN (Diagnostic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(proteomics and bioinformatics approaches for identification of serum biomarkers to detect breast ***cancer***)
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L9 ANSWER 6 OF 11 CA COPYRIGHT 2004 ACS on STN
AN 137:199271 CA
ED Entered STN: 26 Sep 2002
TI Serum protein fingerprinting coupled with a pattern-matching algorithm distinguishes prostate ***cancer*** from benign prostate hyperplasia and healthy men
AU Adam, Bao-Ling; Qu, Yinsheng; Davis, John W.; Ward, Michael D.; Clements, Mary Ann; Cazares, Lisa H.; Semmes, O. John; Schellhammer, Paul F.; Yasui, Yutaka; Feng, Ziding; Wright, George L., Jr.
CS Departments of Microbiology and Molecular Cell Biology, Virginia Prostate Center, Eastern Virginia Medical School, Norfolk, VA, 23501, USA
SO Cancer Research (2002), 62(13), 3609-3614
CODEN: CNREA8; ISSN: 0008-5472
PB American Association for Cancer Research
DT Journal
LA English
CC 14-1 (Mammalian Pathological Biochemistry)
Section cross-reference(s): 3
AB The prostate-specific antigen test has been a major factor in increasing awareness and better patient management of prostate ***cancer*** (PCA), but its lack of specificity limits its use in diagnosis and makes for poor early detection of PCA. The objective of our studies is to identify better biomarkers for early detection of PCA using protein profiling technologies that can simultaneously resolve and analyze multiple proteins. Evaluating multiple proteins will be essential to establishing signature proteomic patterns that distinguish ***cancer*** from noncancer as well as identify all genetic subtypes of the ***cancer*** and their biol. activity. In this study, we used a protein biochip ***surface*** ***enhanced*** ***laser*** ***desorption*** / ***ionization*** mass spectrometry approach coupled with an artificial intelligence learning algorithm to differentiate PCA from noncancer cohorts. ***Surface*** ***enhanced*** ***laser*** ***desorption*** / ***ionization*** mass spectrometry protein profiles of serum from 167 PCA patients, 77 patients with benign prostate hyperplasia, and 82 age-matched unaffected healthy men were used to train and develop a decision tree classification algorithm that used a nine-protein mass pattern that correctly classified 96% of the samples. A blinded test set, sepd. from the training set by a stratified random sampling before the anal., was used to det. the sensitivity and specificity of the classification system. A sensitivity of 83%, a specificity of 97%, and a pos. predictive value of 96% for the study population and 91% for the general population were obtained when comparing the PCA vs. non- ***cancer*** (benign prostate hyperplasia/healthy men) groups. This high-throughput proteomic classification system will provide a highly accurate and innovative approach for the early detection/diagnosis of PCA.
ST protein fingerprinting PSA diagnosis prostate ***cancer*** hyperplasia
IT Prostate gland, disease
(benign hyperplasia; serum protein fingerprinting and prostate-specific antigen as early ***diagnostic*** and prognostic markers for prostate ***cancer*** and benign prostate hyperplasia in men)
IT Proteins
RL: BSU (Biological study, unclassified); DGN (Diagnostic use); BIOL (Biological study); USES (Uses)
(blood, fingerprinting; serum protein fingerprinting and prostate-specific antigen as early ***diagnostic*** and prognostic markers for prostate ***cancer*** and benign prostate hyperplasia in men)
IT Diagnosis
(***cancer*** ; serum protein fingerprinting and prostate-specific antigen as early ***diagnostic*** and prognostic markers for prostate ***cancer*** and benign prostate hyperplasia in men)
IT Prostate gland, neoplasm
(carcinoma; serum protein fingerprinting and prostate-specific antigen as early ***diagnostic*** and prognostic markers for prostate ***cancer*** and benign prostate hyperplasia in men)
IT Diagnosis
(genetic; serum protein fingerprinting and prostate-specific antigen as early ***diagnostic*** and prognostic markers for prostate ***cancer*** and benign prostate hyperplasia in men)
IT Aging, animal

DNA fingerprinting
Human
Prognosis
(serum protein fingerprinting and prostate-specific antigen as early ***diagnostic*** and prognostic markers for prostate ***cancer*** and benign prostate hyperplasia in men)
IT Prostate-specific antigen
RL: BSU (Biological study, unclassified); DGN (Diagnostic use); BIOL (Biological study); USES (Uses)
(serum protein fingerprinting and prostate-specific antigen as early ***diagnostic*** and prognostic markers for prostate ***cancer*** and benign prostate hyperplasia in men)
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L9 ANSWER 7 OF 11 CA COPYRIGHT 2004 ACS on STN
AN 136:383614 CA
ED Entered STN: 13 Jun 2002
TI ***Cancer*** proteomics: New developments in clinical chemistry

AU Rai, A. J.; Chan, D. W.
CS Dept. of Pathology, Div. of Clinical Chemistry, The Johns Hopkins University School of Medicine, Baltimore, MD, 21287, USA

SO Laboratoriumsmedizin (2001), 25(9-10), 399-403
CODEN: LABOD3; ISSN: 0342-3026
PB Blackwell Wissenschafts-Verlag GmbH
DT Journal; General Review
LA English

CC 14-0 (Mammalian Pathological Biochemistry)

AB A review. The entire protein complement of a cell is termed the proteome. "Proteomics" is defined as the systematic expression of diverse properties of proteins in a cell. Proteomic methodologies can detect protein modifications, which occur after protein synthesis. The anal. of the proteome thus provides useful information, which can be used for the identification and screening of ***diagnostic*** markers, and is relevant for the understanding of tumor-progression. In past years, the most widely used tool of proteome-anal. was 2D-gel electrophoresis. Today, new methods are available, which are based on biochip technol. High affinity surface-binding arrays can analyze epitopes of complex protein matrixes and specify functional aspects of tumor-progression. After initial isolation, the sepd. proteins are identified by mass spectrometry based techniques such as MALDI (matrix assisted laser desorption ionization) or SELDI (***surface*** ***enhanced*** ***laser*** ***desorption*** ***ionization***) - TOF (time of flight). This review focuses on new developments in proteomics, including SELDI, and describes applications of these methods for the search of new "protein signatures" in ***cancer*** research. It is expected that the advancements of proteomics-techniques will help to classify human ***cancer*** by mol. rather than morphol. characteristics.

ST review human ***cancer*** marker proteome
IT DNA microarray technology
Human
Mass spectrometry
Neoplasm
Tumor markers
(***cancer*** proteomics, new developments in clin. chem.)
IT Proteome

(Properties); BIOL (Biological study); USES (Uses)
(***cancer*** proteomics, new developments in clin. chem.)
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L9 ANSWER 8 OF 11 CA COPYRIGHT 2004 ACS on STN
AN 136:365982 CA
ED Entered STN: 06 Jun 2002
TI An integrated approach utilizing artificial neural networks and SELDI mass spectrometry for the classification of human tumors and rapid identification of potential biomarkers
AU Ball, G.; Mian, S.; Holding, F.; Allibone, R. O.; Lowe, J.; Ali, S.; Li, G.; McCardle, S.; Ellis, I. O.; Creaser, C.; Rees, R. C.
CS Department of Life Sciences, Nottingham Trent University, Nottingham, NG11 8NS, UK
SO Bioinformatics (2002), 18(3), 395-404
CODEN: BOINFP; ISSN: 1367-4803
PB Oxford University Press
DT Journal
LA English
CC 9-5 (Biochemical Methods)
Section cross-reference(s): 14
AB Motivation: MALDI mass spectrometry is able to elicit macromol. expression data from cellular material and when used in conjunction with Ciphergen protein chip technol. (also referred to as SELDI- ***Surface*** ***Enhanced*** ***Laser*** ***Desorption*** / ***Ionization***), it permits a semi-high throughput approach to be taken with respect to sample processing and data acquisition. Due to the large array of data that is generated from a single anal. (8-10 000 variables using a mass range of 2-15 kDa-this paper) it is essential to implement the use of algorithms that can detect expression patterns from such large vols. of data correlating to a given biol./pathol. phenotype from multiple samples. If successful, the methodol. could be extrapolated to larger data sets to enable the identification of validated biomarkers correlating strongly to disease progression. This would not only serve to enable tumors to be classified according to their mol. expression profile but could also focus attention upon a relatively small no. of mols. that might warrant further biochem./mol. characterization to assess their suitability as potential therapeutic targets. Results: Using a multi-layer perceptron Artificial Neural Network (ANN) (Neuroshell 2) with a back propagation algorithm we have developed a prototype approach that uses a model system (comprising five low and seven high-grade human astrocytomas) to identify mass spectral peaks whose relative intensity values correlate strongly to tumor grade. Analyzing data derived from MALDI mass spectrometry in conjunction with Ciphergen protein chip technol. we have used relative importance values, detd. from the wts. of trained ANNs, to identify masses that accurately predict tumor grade. Implementing a three-stage procedure, we have screened a population of approx. 100 000-120 000 variables and identified two ions (m/z values of 13 454 and 13 457) whose relative intensity pattern was significantly reduced in high-grade astrocytoma. The data from this initial study suggests that application of ANN-based approaches can identify mol. ion patterns which strongly assoc. with disease grade and that its application to larger cohorts of patient material could potentially facilitate the rapid identification of validated biomarkers having significant clin. (i.e. ***diagnostic*** /prognostic) potential for the field of ***cancer*** biol.
ST artificial neural network SELDI mass spectrometry tumor biomarker
IT Diagnosis
(agents; integrated approach utilizing artificial neural networks and SELDI mass spectrometry for classification of human tumors and rapid identification of potential biomarkers)
IT Algorithm
Animal tissue
Biomarkers (biological responses)
Computer program
Human
Microarray technology

Sample preparation
(integrated approach utilizing artificial neural networks and SELDI mass spectrometry for classification of human tumors and rapid identification of potential biomarkers)

IT Proteins
RL: ANT (Analyte); DGN (Diagnostic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(integrated approach utilizing artificial neural networks and SELDI mass spectrometry for classification of human tumors and rapid identification of potential biomarkers)

IT Astrocyte
(neoplasm, astrocytoma; integrated approach utilizing artificial neural networks and SELDI mass spectrometry for classification of human tumors and rapid identification of potential biomarkers)

IT Simulation and Modeling, physicochemical
(neural network; integrated approach utilizing artificial neural networks and SELDI mass spectrometry for classification of human tumors and rapid identification of potential biomarkers)

IT Laser ionization mass spectrometry
(photodesorption, matrix-assisted; integrated approach utilizing artificial neural networks and SELDI mass spectrometry for classification of human tumors and rapid identification of potential biomarkers)

IT Laser ionization mass spectrometry
(photodesorption, surface-enhanced; integrated approach utilizing artificial neural networks and SELDI mass spectrometry for classification of human tumors and rapid identification of potential biomarkers)

IT Laser desorption mass spectrometry
(photoionization, matrix-assisted; integrated approach utilizing artificial neural networks and SELDI mass spectrometry for classification of human tumors and rapid identification of potential biomarkers)

IT Laser desorption mass spectrometry
(photoionization, surface-enhanced; integrated approach utilizing artificial neural networks and SELDI mass spectrometry for classification of human tumors and rapid identification of potential biomarkers)

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L9 ANSWER 9 OF 11 CA COPYRIGHT 2004 ACS on STN
AN 136:365893 CA
ED Entered STN: 06 Jun 2002
TI The SELDI-TOF MS approach to proteomics: Protein profiling and biomarker identification

AU Issaq, Haleem J.; Veenstra, Timothy D.; Conrads, Thomas P.; Felschow, Donna
CS SAIC-Frederick, Inc., National Cancer Institute at Frederick, Frederick, MD, 21702, USA

587-592
CODEN: BBRCA9; ISSN: 0006-291X
PB Elsevier Science
DT Journal; General Review
LA English
CC 9-0 (Biochemical Methods)
AB A review. The need for methods to identify disease biomarkers is underscored by the survival-rate of patients diagnosed at early stages of ***cancer*** progression. ***Surface*** ***enhanced*** ***laser*** ***desorption*** / ***ionization*** time-of-flight mass spectrometry (SELDI-TOF MS) is a novel approach to biomarker discovery that combines two powerful techniques: chromatog. and mass spectrometry. One of the key features of SELDI-TOF MS is its ability to provide a rapid protein expression profile from a variety of biol. and clin. samples. It has been used for biomarker identification as well as the study of protein-protein, and protein-DNA interaction. The versatility of SELDI-TOF MS has allowed its use in projects ranging from the identification of potential ***diagnostic*** markers for prostate, bladder, breast, and ovarian ***cancers*** and Alzheimer's disease, to the study of biomol. interactions and the characterization of post-translational modifications. In this minireview we discuss the application of SELDI-TOF MS to protein biomarker discovery and profiling.
ST review SELDI TOF MS protein profiling biomarker
IT Biomarkers (biological responses)
Neoplasm
Time-of-flight mass spectrometry
(SELDI-TOF MS approach to proteomics)
IT Proteins
RL: ANT (Analyte); DGN (Diagnostic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(SELDI-TOF MS approach to proteomics)
IT Diagnosis
(agents; SELDI-TOF MS approach to proteomics)
IT Laser ionization mass spectrometry
(photodesorption, surface-enhanced; SELDI-TOF MS approach to proteomics)
IT Laser desorption mass spectrometry
(photoionization, surface-enhanced; SELDI-TOF MS approach to proteomics)
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L9 ANSWER 10 OF 11 CA COPYRIGHT 2004 ACS on STN
AN 136:34118 CA
ED Entered STN: 10 Jan 2002
TI Development of a novel proteomic approach for the detection of transitional cell carcinoma of the bladder in urine
AU Vlahou, Antonia; Schellhammer, Paul F.; Mendrinos, Savvas; Patel, Keyur; Kondylis, Filippos I.; Gong, Lei; Nasim, Suhail; Wright, George L., Jr.
CS Departments of Microbiology and Molecular Cell Biology, Eastern Virginia Medical School, Norfolk, VA, 23507, USA
SO American Journal of Pathology (2001), 158(4), 1491-1502
CODEN: AJPAA4; ISSN: 0002-9440
PB American Society for Investigative Pathology
DT Journal
LA English

Section cross-reference(s): 14

AB Development of noninvasive methods for the diagnosis of transitional cell carcinoma (TCC) of the bladder remains a challenge. A ProteinChip technol. (***surface*** ***enhanced*** ***laser*** ***desorption*** / ***ionization*** time of flight mass spectrometry) has recently been developed to facilitate protein profiling of biol. mixts. This report describes an exploratory study of this technol. as a TCC ***diagnostic*** tool. Ninety-four urine samples from patients with TCC, patients with other urogenital diseases, and healthy donors were analyzed. Multiple protein changes were reproducibly detected in the TCC group, including five potential novel TCC biomarkers and seven protein clusters (mass range, 3.3 to 133 kDa). One of the TCC biomarkers (3.4 kDa) was also detected in bladder ***cancer*** cells procured from bladder barbotage and was identified as defensin. The TCC detection rates provided by the individual markers ranged from 43 to 70% and specificities from 70 to 86%. Combination of the protein biomarkers and clusters, increased significantly the sensitivity for detecting TCC to 87% with a specificity of 66%. Interestingly, this combinatorial approach provided sensitivity of 78% for detecting low-grade TCC compared to only 33% of voided urine or bladder-washing cytol. Collectively these results support the potential of this proteomic approach for the development of a highly sensitive urinary TCC ***diagnostic*** test.

ST development proteomic detection transitional cell carcinoma bladder urine

IT Diagnosis
(***cancer*** ; development of a novel proteomic approach for detection of transitional cell carcinoma of bladder in urine)

IT Animal cell
Tumor markers
Urine analysis
(development of a novel proteomic approach for detection of transitional cell carcinoma of bladder in urine)

IT Proteins
Proteome
RL: ANT (Analyte); DGN (Diagnostic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(development of a novel proteomic approach for detection of transitional cell carcinoma of bladder in urine)

IT Urogenital tract
(disease; development of a novel proteomic approach for detection of transitional cell carcinoma of bladder in urine)

IT Time-of-flight mass spectrometry
(***surface*** ***enhanced*** ***laser*** ***desorption*** / ***ionization*** ; development of a novel proteomic approach for detection of transitional cell carcinoma of bladder in urine)

IT Bladder, neoplasm
(transitional cell carcinoma; development of a novel proteomic approach for detection of transitional cell carcinoma of bladder in urine)

IT 103220-14-0, Defensin
RL: ANT (Analyte); DGN (Diagnostic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(development of a novel proteomic approach for detection of transitional cell carcinoma of bladder in urine)

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L9 ANSWER 11 OF 11 CA COPYRIGHT 2004 ACS on STN
AN 135:192394 CA
ED Entered STN: 20 Sep 2001
TI Quantitation of serum prostate-specific membrane antigen by a novel protein biochip immunoassay discriminates benign from malignant prostate disease
AU Xiao, Zhen; Adam, Bao-Ling; Cazares, Lisa H.; Clements, Mary Ann; Davis, John W.; Schellhammer, Paul F.; Dalmasso, Enrique A.; Wright, George L., Jr.
CS Department of Microbiology and Molecular Cell Biology and Virginia Prostate Center, Eastern Virginia Medical School, Norfolk, VA, 23507, USA
SO Cancer Research (2001), 61(16), 6029-6033
CODEN: CNREA8; ISSN: 0008-5472
PB American Association for Cancer Research
DT Journal
LA English
CC 9-10 (Biochemical Methods)
Section cross-reference(s): 14
AB The lack of a sensitive immunoassay for quantitating serum prostate-specific membrane antigen (PSMA) hinders its clin. utility as a ***diagnostic*** /prognostic biomarker. An innovative protein biochip immunoassay was used to quantitate and compare serum PSMA levels in healthy men and patients with either benign or malignant prostate disease. PSMA was captured from serum by anti-PSMA antibody bound to ProteinChip arrays, the captured PSMA detected by ***surface*** - ***enhanced*** ***laser*** ***desorption*** / ***ionization*** mass spectrometry, and quantitated by comparing the mass signal integrals to a std. curve established using purified recombinant PSMA. The av. serum PSMA value for prostate ***cancer*** (623.1 ng/mL) was significantly different ($P < 0.001$) from that for benign prostate hyperplasia (117.1 ng/mL) and the normal groups (age <50, 272.9 ng/mL; age >50, 359.4 ng/mL). These initial results suggest that serum PSMA may be a more effective biomarker than prostate-specific antigen for differentiating benign from malignant prostate disease and warrants addnl. evaluation of the ***surface*** - ***enhanced*** ***laser*** ***desorption*** / ***ionization*** PSMA immunoassay to det. its ***diagnostic*** utility.
ST prostate membrane antigen detn protein biochip immunoassay
IT Diagnosis
(agents; serum prostate-specific membrane antigen detn. by protein biochip immunoassay)
IT Prostate gland
(disease; serum prostate-specific membrane antigen detn. by protein biochip immunoassay)
IT Prostate gland
(neoplasm; serum prostate-specific membrane antigen detn. by protein biochip immunoassay)
IT Biotechnology
Blood serum
Hyperplasia
Immunoassay
(serum prostate-specific membrane antigen detn. by protein biochip

IT Prostate-specific antigen
RL: ANT (Analyte); ANST (Analytical study)
(serum prostate-specific membrane antigen detn. by protein biochip immunoassay)
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